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ZINC 2 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
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01-FEB-1994
01-JUN-1994
15-JUN-2002
                           MEDLINE=93094198; PubMed=1460002; Mg K., Ye R., Wu X.-C., Wong S.-L "Sorbitol dehydrogenase from Back characterization, and gene cloning characterization.
                                                                                                                                                      SEQUENCE FF
STRAIN=168;
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NCBI_TaxID=1423;
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SGD; SO000057; YAL061W.
InterPro; IPR002328; ADH_Zinc.
InterPro; IPR002085; Adh_zn_family.
Pfam; PF00107; Adh_Zinc; 1.
PROSITE; P500059; ADH_ZINC; 1.
Hypothetical protein; Oxidoreductase;
Hypothetical protein; Oxidoreductase;
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   on, and gene cloning."
267:24989-24994(1992)
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Pred. No. 9.2e<sup>-</sup>
71; Mismatches
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Bacillus
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ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (SECOND ATOM) (BY SIMILARITY).
ZINC (SECOND ATOM) (BY SIMILARITY).
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ZINC (CATALYTIC) (BY SIMILARITY).
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MEDLINE-98044033;

PubMed=9384377;

SEQUENCE FROM N.A.

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RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

RA Gliseppi G., Guy B.J., Haga K., Haicch J., Harwood C.R., Henaut A.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Hilbert H., Kasanata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,

RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,

RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Park S.H.,

RA Parro V., Pohl T.M., Ogawa K., Ogawara A., Oudega B., Park S.H.,

RA Parro V., Pohl T.M., Portetelle D., Porvollik S., Prescott A.M.,

RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,

RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,

RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,

RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,

RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,

RA Tosato V., Uchlyama S., Vandenbol M., Vannier F., Vassarotti A.,

RA Viari A., Wambutt R., Wedler E., Wedler H., Weltzenegger T.,

RA Viari A., Walker E., Wedler E., Yoshikawa H., Danchin A.,

The complete genome sequence of the Gram-positive bacterium Bacillus
                               Query Match
   Best Local Similarity
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EMBL; 299107; CAB12434.1; -.
PIR; A45052; A45052.
HSSP; P07846; 1SDG.
SUBCLIST; BG10177; gutB.
InterPro; IPR002328; ADH_zinc.
InterPro; IPR002085; Adh_zn_family.
InterPro; IPR002085; NAD_binding.
Pfam: P87001077. Adh_zinc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROSITE; PS00059; ADH_ZINC; 1.
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ZINC (SECOND ATOM) (BY SIMILARITY).
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01-JUL-1993
15-JUL-1999
                                                                                                                                      STRAIN-Tokai X Asahi; TISSUE-Fat body;
MEDLINE-97087160; PUBMed-8933178;
Niimi T., Yamashita O., Yaginuma T.;
"Structure of the Bombyx sorbitol dehydrogenase
alternative use of the promoter.";
Insect Mol. Biol. 5:269-280(1996).
-i- CATALYTIC ACTIVITY; L-iditol + NAD(+) - L-so
-i- COFACTOR: ZINC.
                                                                                                                                                                                                                                                                               sorbitol dehydrogenase. diapause eggs."; Eur. J. Biochem. 213:117
                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Mandibulata; Insecta; Pterygota; Neoptera; Endopterygota; Ditrysia; Bombycoidea; Bombycidae; Bombyx.
                                          between
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        "A cold-inducible Bombyx
                                                                                                                                                                                                                                                                                                                                                       MEDLINE-93279312;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bombyx mori (Silk moth).
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           s SWISS-PROT entry is copyright. It is produced through a collal ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
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ta O., Yaginuma T.;
Bombyx gene encoding a protein similar to mammalian
enase. Yolk nuclei-dependent gene expression in
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Last
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Best Local
Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Barooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
                                                                                                                                                                                                                                                                                                 _SCHPO
                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                               P36624:
01-JUN-1994 (Rel. 29, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative sorbitol dehydrogenase (EC 1.1.1.14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METAL
SEQUENCE
                                                                                        MEDLINE=21848401; PubMed=11859360;
                                                                                                       STRAIN-97
                                                                                                                                                       Schizosaccharomyces
                                                                                                                                                                                                        2-dehydrogenase) (Protein TMS1 OR SPC1773.05C.
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PROSITE; PS00059; ADH_ZINC; 1.
Oxidoreductase; Zinc; NAD.
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HSSP;
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InterPro; IPR002085; Adh_zn_family.
InterPro; IPR000205; NAD_binding.
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L; D66906; BAA11030
; S32484; S32484.
P; P07846; ISDG.
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348 AA;
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license@isb-sib.ch).
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ZINC (CATALYTIC) (B)
ZINC (CATALYTIC) (B)
ZINC (CATALYTIC) (B)
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Pred. No. 2.1
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RRA Cliver K., O Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RRA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RRA Rutherford K., Simmonds M., Squares R., Squares S., Stevens K.,
RRA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RRA Faylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RRA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RRA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Wheller-Auer S.,
RRA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RRA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RRA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RRA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RRA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RRA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RRA Goffeau A., Cadieu E., Dreano S., Hunt C., Moore K., Hurst S.M.,
RRA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RRA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RRA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RRA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RRA Daminguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RRA Abpakovski G. V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
RNA L21
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Oliver K.,
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                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Magner P., Grimaldi M., Jenkins J.R.;
"Putative dehydrogenase tms1 suppresses
p53 tumour mutant in fission yeast.";
Eur. J. Biochem. 217:731-736(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94039112; PubMed=8223615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 5-360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: L-iditol + NAD(+)
COTACTOR: ZINC (BY SIMILARITY).
SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
SIMILARITY: BELONGS TO THE ZINC-CONTAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: SUPPRESSES GROWTH ARREST IN FISSION YEAST.
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Query Match Best Local S Matches 109 METAL SEQUENCE PIR; METAL PROSITE; PS0005 Oxidoreductase; METAL InterPro; InterPro; [nterPro; \$35981; \$35981. \$38345; \$38345. Pro; IPR002328; ADH_zinc.
Pro; IPR002085; Adh_zn_family.
Pro; IPR000205; NAD_binding.
PF00107; adh_zinc; 1. P07846; 1SDG PS00059; ADH uctase; Zinc; 153 360 42 67 AA; ; ADH_ZINC; Zinc; NAD. 38851 MW; 18.0%; 29.7%; Score 362; DB Pred. No. 1.3e 59; Mismatches ZINC ZINC ZINC INC (CATALYTIC) (BY SIMILARITY).
INC (CATALYTIC) (BY SIMILARITY).
INC (CATALYTIC) (BY SIMILARITY).
ADEB3DDBA163224C CRC64; 362; DB 1; |.3e-20; nes 161; Length

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ESAGVVVEVGKGVSSLKPGDPVAVEPGCVCR

EFSGTVVEVGSGVTSVKPGDRVAVEATSHCSDRSRYKDTVAQDLGLCMACQSGSPNCCAS

LCDYCRSGRYNLCPH

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135 67

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EDRPGQTLTDDHQVKVAIKATGICGSDVHYWKEGGIGDFILKK

PMILGH

ETVPEPEIKNPNDVKIKVSYCGICGTDLKEFTYSGGPVFFPKQGTKDKISGYELPLCPGH

16

109;

Conservative

59;

Indels

38;

Gaps

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360;

Similarity

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136 83

LSFCGLGGASGGFAEYVVYGEDHMVKLPDSIPDDIGALVEPISVAWHAVERARFQPGQTA

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01-JUN-1994 (Rel. 29, Last sequence update)
115-JUL-1999 (Rel. 38, Last annotation update)
Sorbitol dehydrogenase (EC 1.1.1.14) (L-iditol 2
SOR1 OR SDH1 OR YUR159W OR J2395.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Saccharomycetaceae; Saccharomycetaremycetales;
                                                                                                                      EMBL; L11039; AAA35027.1;
EMBL; Z49659; CAA89692.1;
HSSP; P07846; 1SDG.
                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as greement and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                         Wedler H., Underwood A.P., Louis E.J., Wambutt Submitted (SEP-1995) to the EMBL/GenBank/DDBJ c-1- CATALYTIC ACTIVITY: L-1ditol + NAD(+) - L-5
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-20 FROM N.A. Huang M.-E., Chuat J.-C., Gar Submitted (SEP-1995) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94171068; PubMed=8125328;
Sarthy A.V., Schopp C., Idler K.B.;
"Cloning and sequence determination of the gene
dehydrogenase from Saccharomyces cerevisiae.";
Gene 140:121-126(1994).
                                         Pfam; PF00107;
PROSITE; PS000
                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
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                             Oxidoreductase;
                                                     InterPro; IPR000205; NAD_binding.
Pfam; PF00107; adh_zinc; 1.
                                                                                InterPro; IPR002328; ADH_zinc.
InterPro; IPR002085; Adh_zn_family.
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                                                                                                            S0003920; SOR1.
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                            Zinc;
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Best Local
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         MEDLINE-97251357; PubMed-9097039;
Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
Rasai H., Rashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura
Makade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., S
Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,
Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horluchi T.,
Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horluchi T.,
"A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.
DNA Res. 3:363-377(1996).
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SEQUENCE
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                                                                                                                                                                                                                Gregor J., Davis N.W., Kirkpatrick H.A., Mau B., Shao Y.;
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ZINC (CATALYTIC) (BY SIN
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EMBL; A16166; CAA01269.1;
PIR; S13529; S13529.
HSSP; P07846; ISDG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Koetter P., Amore R., Hollenberg C.P., Ciriacy M.; "Isolation and characterization of the Pichia stipitis dehydrogenase gene, XYL2, and construction of a xylose-saccharomyces cerevisiae transformant.";
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00107; adh_zinc; 1. PROSITE; PS00059; ADH_ZINC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- PATHWAY: D-xylose degradation.
-!- INDUCTION: BY XYLOSE. REPRESSED BY GLUCOSE.
-!- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Persson B., Hallborn J., Walfridsson Keraenen S., Penttilae M., Joernvall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93279386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY TO OTHER ZINC-ALCOHOL DEHYDROGENASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91168296; PubMed=2127555;
 225
                                 239
                                                                  165
                                                                                                  181
                                                                                                                                   105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Dual relationships of xylitol and alcohol dehydrogenases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4924;
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                                                                                                                                                                                                                                                                                           NDIRYSETVPEPEIKNPNDVKIKVSYCGICGTDLKEFTYSGGPVFFPKQGTKDKISGYEL
 TFNSKT-GGSEELIKAFGGNVP--
                                                                                                                                 GHYNLCPHMAFAATPNSKEGEPNPPGTLCKYFKSPEDFLVKLPDHVSLELGALVEPLSVG
                               VFDPSTCDDANAVLKAM----VPENEGFHAAFDCSGVPQTFTTSIVATGPSGIAVNVAVWG
                                                                VHASKLGSVAFGDYVAVFGAGPVGLLAAAVAKTFGAKGVIVVDIFDNKLKMAKDIGAATH
                                                                                                WHAVERAREQPGQTALVLGGGPIGLATILALQGHHAGKIVCSEPALIRRQFAKELGA--E
                                                                                                                                                                  GSPNCCASLSFC-----GLGGASGGFAEYVVYGEDHMVKLPDSIPDDIGALVEPISVA
                                                                                                                                                                                                  TKPMVLGHESAGTVVQVGKGVTSLKVGDNVAIEP----GIPSRFSDEY--
                                                                                                                                                                                                                   --PLCPGHEFSGTVVEVGSGVTSVKPGDRVAVEATSHCSDRSRYKDTVAQDLGLCMACQS
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IPR002085; Adh_zn_family.
IPR000205; NAD_binding.
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183
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Xylose metabolism;
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Q00796; Q1668; Q9UMD6;
Q1-APR-1993 (Rel. 25, Creat
Q1-CCT-1996 (Rel. 34, Last
15-JUN-2002 (Rel. 41, Last
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94375058; PubMed-8088829;
Lee F.K., Cheung M.C., Chung S.;
"The human sorbitch dehydrogenase gene: cDN
determination, and mapping by fluorescence
Genomics 21:354-358(1994).
                        This SWISS-PROT entry is copyright. It is produced through a collaboration-between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                         sorbitol
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                                                                                                                                                                                                                                                                                                                 MEDLINE-97326004; PubMed-9183016; Carr I.M., Markham A.F., Coletta P.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-95301293; PubMed-7782086;
Iwata T., Popescu N.C., Zimonjic D.B.,
Vaca G., Rodriguez I.R., Carper D.,
Vaca G., Rodriguez I.R.,
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"Varlability within mammalian sorbitol
structure of the human liver enzyme.",
Eur. J. Biochem. 186:543-550(1989).
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Biochem. 245:760-767(1997).
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annotation update)
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DHSO_BACHD
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AC Q9Z9UI
DT 16-OCT
DT 16-OCT
DT 16-OCT
DE Sorbit
DE (Gluci

Q9Z9U1; DHSO_BACHD

STANDARD;

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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Sorbitol dehydrogenase (EC 1.1.1.14) (L-iditol (Glucitol dehydrogenase).

2-dehydrogenase)

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                243
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223 ISKESPQETARKV----EGLLGCKPEVTIECTGAEASIQAGIYATRSGGTLVLVGL
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                                                                                                        KISGYELPLCPGHEFSGTVVEVGSGVTSVKPGDRVAVEATSHCSDRSRYKDTVAQDLGLC
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                                                                 --CKMGRYNLSPSIFFCATPPDDGNLCRFYKHNAAFCYKLPDNVTFEEGALIEPLSVGIH
                                                                        MACQSGSPNCCASLSFCGLGGASGGFAEYVVYGEDHMYKLPDSIPDDIGALVEPISVAWH 182
                STCDDANAVLKAMVPENEGF-----HAAFDCSGVPQTFTTSIVATGPSGIAVNVAV
                                ACRRGGVTLGHKVLVCGAGPIGMVTLLVAKAMGAAQVVVTDLSATRLSKAKEIGADLVLQ
                                                AVERARFOPGOTALVLGGGPIGLATILALQGHHAGKIVCSEPALIRRQFAKELGAEVFDP
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M -> E (

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C (IN REF. 1).
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METAL 39
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-!- FUNCTION: REDUCES GLUCITOL TO FRUCTOSE (BY:
-!- CATALYTIC ACTIVITY: L-iditol + NAD(+) = L-s:
-!- COFACTOR: ZINC (BY SIMILARITY).

-!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. Their use by non-profit institutions as long a modified and this statement is not removed.
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InterPro; IPR002085; Adh_zn_f;
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PROSITE; PS00059; ADH_ZINC;
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Fuji F., Hirama C., Nakamura Y., Ogasawara
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Masul N., Fuji F., Takaki Y., Inoue A.,
"Sequencing of three lambda clones from
Bacillus sp. strain C-125.";
Extremophiles 3:29-34(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C-125 / JCM 9153;
MEDLINE=99184646; PubMed=10086842;
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Bacteria; Firmicutes;
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DLGLCMACQSGSPNCCASLSFCGLGG-ASGGFAEYVVYGEDHMVKLPDSIPDDIGALVEP
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WC (CAPALYTIC) (BY SIMILARITY).
WC (SECOND ATOM) (BY SIMILARITY).
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., Horikoshi K.;
om the genome of alkaliphilic
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9.2e-19;
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EMBL; AE000272; EMBL; D90820; BA EMBL; D90821; BA HSSP; P07846; 1S

BAA15565.1; BAA15572.1; 1SDG.

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InterPro;
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IPR002328; ADH_zinc.
IPR002085; Adh_zn_family.
IPR000205; NAD_binding.

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PF00107;

adh_zinc;

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MEDLINE-97251357; PubMed-9097039;
Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
Kasai H., Kashimoto K., Mixi T., Motomura
Makino K., Mixi T., Mixobuchi K., Mori H., Mori T., Motomura
Makade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., S
Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,
Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.,
"A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.
                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                               DNA Res. 3:363-377(1996).
-!- COFACTOR: ZINC (Potential).
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Riley M., Collado-Vides J., Glasner J.D., Rode
Gregor J., Davis N.W., Kirkpatrick H.A., Goeder
Mau B., Shao Y.;
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STRAIN=K12 / MG1655;
MEDLINE=97426617; Pu
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YDJJ OR B1774
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01-NOV-1997 (Rel. 35, Last send)
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Hypothetical zinc-type alcohol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complete genome sequence of 
nce 277:1453-1474(1997).
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Mammalia; Eutheria; (
Bovidae; Caprinae; Ov
NCBI_TaxID=9940;
SIMILARITY TO ZINC ALCOHOL DEHYDROGENASES.
MEDLINE-84158592; PubMed-6368230;
JOERNVA11 H., VON BAhr-LindStrom H., Jeffery J
"Extensive variations and basic features in the
dehydrogenase-sorbitol dehydrogenase family.";
Eur. J. Biochem. 140:17-23(1984).
                                                                                                                                                                                                                DHSO_SHEEP
P07846;
                                                                 enzyme.";
Eur. J. B
                                                                                                                                                                            01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Sorbitol dehydrogenase (EC 1.1.1.14) (L-iditol
                                                                              MEDLINE-84158607; PubMed-6705798;
Jeffery J., Cederlund E., Joernva
"Sorbitol dehydrogenase. The prim
                                                                                                        TISSUE-Liver;
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                                                                Biochem. 140:7-16(1984).
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ZINC (SECOND ATOM) (BY SIMILARITY).
F8E2172184625A3B CRC64;
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PDB; 1SDG; 15-OCT-94.
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Eklund H., Horjales E., Jornvall H., Branden
"Molecular aspects of functional differences
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SIMILARITY: BELONGS TO
FAMILY.
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re; PS00059; ADH_zINC; 1.
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IPR002085; Adh_zn_family.
IPR000205; NAD_binding.
 zinc;
NAD;
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( SIMILARITY).
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1 DHSO_RAT
2 P27867;
1 01-AUG-1992 (Rel. 23, Created)
2 01-NOV-1997 (Rel. 35, Last sequence update)
2 16-OCV-2001 (Rel. 40, Last annotation update)
2 corbitol dehydrogenase (EC 1.1.1.14) (L-iditc
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Best Local
                               between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. Their
use by non-profit institutions as long a
modified and this statement is not removed.
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SEQUENCE
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Eur. J. Biochem. 198:761-765(1991).
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"Sorbitol dehydrogenase.
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Mammalia; Eutheria;
                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY:
-!- COFACTOR: ZINC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-terminal end.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coding for a
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                                                                                                                                                                                                                                                                 SUBUNIT: HOMOTETRAMER.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY USE OF ALTERNATIVE INITIATION.
SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
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97; Conserv
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354 AA;
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TIVITY: L-iditol + NAD(+) =
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                                                                                                                             Institute of Bioinformatics
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37831 MW;
license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.7%;
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D5FE56BC06F87389 CRC64;
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(L-iditol
                                                       There are no restrictions ong as its content is in
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                                                                                                                                                                                                                                                                                                                                                                                                                                            L-sorbose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muridae;
                           Usage
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t the
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Best Local
                                                                                                                                            DHSO_MOUSE
Q64442;
Q1-NOV-1997
Q1-NOV-1997
Q1-NOV-1997
SEQUENCE FROM N.A. (LONG AND SHORT STRAIN-BALB/C; TISSUE-Liver; MEDLINE-9534564; Pubmed-7601136; Lee F.K., Lee A.Y.W., Lin C.X.F.,
                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                            MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METAL
CONFLICT
SEQUENCE
                                                                                                            (Fragment).
SORD OR SDH1.
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                                                                                                                                  Sorbitol dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           $16132; $16132.
; P07846; 1SDG.
                                                                                                                                                                                                                                                        TAKKGLGLKVMIKCDPND 396
                                                                                                                                                                                                                                                                                                       NLPLVHAAVREVDIKGVFRY-CNTWPMAVSMLASKTLNV---KPLVTHRFPLEKAVEAFE
                                                                                                                                                                                                                                                                                                                                                                                                   CRRGSVSLGNKVLVCGAGPIGIVTLLVAKAMGASQVVVIDLSASRLAKAKEVGADFTIQV
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                                                                                                                                                                                                                                                                                                                             GFMPMSLTYQEKYATGSMCYTVKDFQEVVKALEDGLISLDKARKMITGKVHLKDGVEK---
                                                                                                                                                                                                                                                                                                                                                     AKETPHDIAKKVESVLGSKPE---VTIECTGAESSVQDGIYATHSGGTLVVVGM-GPEMI
                                                                                                                                                                                                                                                                                                                                                                          FDPSTCDDANAVLKAMVPENEGFHAAFDCSGVPQTFTTSIVATGPSGIAVNVAVWGDHPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACQSGSPNCCASLSFCGLGGASGGFAEYVVYGEDHMVKLPDSIPDDIGALVEPISVAWHA
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X74593; CAA52670.1;
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IPR002085; Adh_zn_family.
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                                                                                                                                                                                                                                                                               -GFKQLIEHKENN
                                                                                                                                               (Rel. 35,
(Rel. 35,
(Rel. 41,
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Last sequence update)
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se (EC 1.1.1.14) (L-iditol 2-dehydrogenase)
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SORBITOL DEHYDROGENASE, S
FOR SHORT ISOFORM.
ZINC (CATALYTIC) (BY SIMI
D->T (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 331.5; DB 1
Pred. No. 3.2e-18;
                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> T (IN REF. 2).
42018F127A1856D2 CRC64;
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 Chung
                                      ISOFORMS)
                                                                                                                                                                                              375
  S.S.-M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166;
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(BY SIMILARITY).
(BY SIMILARITY).
  Chung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
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RESULT 15
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CHAIN
      RSPB_ECOLI
P38105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U27014; AAA79043.1; -. HSSP; P07846; 1SDG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:98266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This
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                                                                                                   243 GKETPQEIASKVESLLGSKPE----VTIECTGAESSVQSGIYATHSGGTLVIVGM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MANNITOL, L-IDITOL.
CATALYTIC ACTIVITY: L-iditol + NAD(+) =
COFACTOR: ZINC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oning, sequencing, and determination of the sites of expression se sorbitol dehydrogenase cDNA.";
J. Biochem. 230:1059-1065(1995).
FUNCTION: OXIDIZES SORBITOL AND OTHER POLYOLS SUCH AS XYLITOL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
ALTERNATIVE PRODUCTS: 2 isoforms; a long short form; are produced by alternative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATHWAY: POLYOL PATHWAY
                                                                                                                                                                                       VERARFQPGQTALVLGGGPIGLATILALQGHHAGKIVCSEPALIRRQFAKELGA----EV
                                                                                                                                                                                                                                                                                                                                                                                         LLYYGTNDIRYSETVPEPEIKNPNDVKIKVSYCGICGTDLKEFTYSGGPVFFFKQGTKDK 63
                                                                                                                                                                CRRGSVSLGNKVLVCGAGPVGMVTLLVAKAMGAAQVVVVTDLSASRLTKAKEVGADFTIQV
                                                                                                                                                                                                                                                                    ACQSGSPNCCASLSFCGLGGASGGFAEYVVYGEDHMVKLPDSIPDDIGALVEPISVAWHA 183
                                                                                                                                    FDPSTCDDANAV--LKAMVPENEGFHAAFDCSGVPQTFTTSIVATGPSGIAVNVAV
                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                     YCKIGRYNLTPTIFFCATPPDDGNLCRFYKHNADFCYKLPDSVTFEEGALIEPLSVGIYA
                                                                                                                                                                                                                                                                                                    -----PMVLGHEAAGTVTKVGELVKHLKPGDRVAIE------PGVPREVD--E 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                            93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS00059; ADH_ZINC; 1.
PS00059; ADH_ZINC; 1.
PS00059; ADH_ZINC; Alternative initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR002328; ADH_zinc.
IPR002085; Adh_zn_family.
IPR000205; NAD_binding.
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                    STANDARD;
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ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 329; DB Pred. No. 4.6e 6; Mismatches
                    PRT;
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A Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Sait
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MEDLINB-97456617; PubMed-9278503;
MEDLINB-97456617; PubMed-9278503;
Blatther F.R., Plunkett G. III, Bloch C.A., Perna N.T., Bur
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhav
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose
                                                                                                                                                                                                                                                                                                                            InterPro; IPR002328; ADH_zinc.
InterPro; IPR002085; Adh_zn_family.
Pfam; PF00107; adh_zinc; 1.
PROSITE; PS00059; ADH_ZINC; 1.
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EMBL; AE000254; AAC74652.1; --
EMBL; D90799; BAA15284.1; --
EMBL; D90800; BAA15306.1; --
               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
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STRAIN-K12 / W3110;
MEDLINE-94310441; Pubmed.
Huisman G.W., Kolter R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
Bacteria; Proteobacteria;
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16-OCT-2001 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Exercise Buropean Bioinformatics Institute. There are no rest
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Score

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Length

	Best Local Similarity 27.2%; Pred. No. 2.2e-17; Matches 107; Conservative 57; Mismatches 159; Indels 71; Gaps 16;	
뭐	1 MKGLLYYGTNDIRYSETVPEPEIKNPNDVKIKVSYCGICGTDLKEFTYSGGPVFFPKQ 58	
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_뮹	90 -GHCYPCSIGKPNVCTTLAVLGV-HADGGFSEYAVVPAKNAWKIPEAVADQYAVMIEPFT 147	
-¥.	179 VAWHAVERARFQPGQTALVLGGGPIGLATILALQG-HHAGKIVCSEPALIRRQFAKELGA 237	
	148 IAANVTGHGQPTEND	
. ¥_	238 EVFDPSTCDDANAVLKAMVPENEGFHAAFDCSGVPQTFTTSIVATGPSGIAVN 290	
- B	208 DWAINNSQTPLGEIFTEKGIKPTLIIDAACHPSILKEAVTLASPAAR 254	
_\$	291 VAVWGDHPIGFMPMSLTYQEKYATGSMCYTVKDFQEVVKALEDGLISLDKARKMITGK 348	
	255 IVLMGFSSEPSEVIQQGITGKELSIFSSRLNANK-FPIVIDWLSKGLIKPEKLITHT 310	
. 12	349 VHLKDGVEKGFKQLIEHKENN-V	
₽Đ.	311 FDFQHVADAISLFEQDQKHCCKVLLTESE 339	
Joj Se	Search completed: May 2, 2003, 12:29:29 Job time : 287 secs	

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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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1: sp_archea:*
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1 MKGLLYYGTNDIRYSETVPE.....QLIEHKENNVKILVTPNEVS 380
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sp_organelle:*
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sp_rodent:*
sp_virus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Q8zbq5 yersinia		371	16.8	338	39
		343 .	16.8	339	38
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Q930c9 rhizobium m		343	17.0	343	35
	16 Q8XDU8	358	17.1	345	34
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Q927h6 listeria		343	17.3	348	30
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Q9mbd7 prunus pers		367	17.5	352	27
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09kgb7 bacillus ha		354	17.5	352.5	25
096299 drosophila	_	360	17.7	355.5	24
Q8y9m0 listeria mo		348	17.8	358.5	23
Q9zr22 malus domes		371	17.9	361	22
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Q9maw7 eriobotrya	10 Q9MAW7	371	٠	365	18
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ALIGNMENTS

OSSERS: PRELIMINARY; PRT; 349 AA. AC Q93R65; DT 01-DEC-2001 (TrEMBLrel. 19, Created) DT 01-DEC-2001 (TrEMBLrel. 19, Created) DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) DT 01-DEC-2001 (TrEMBLrel. 21, Last sequence update) DE ACR: DACR: DACR: DACR: DE ACR: DE ACCT: DECACT:	oy p	Qy	ఠ	0		S	DR	DR DR	DR :	U	R.	υ ;	כ ס	Į R	RN	õ	႙	o	0	GN E			ဌ	AC	IJ	Q 2
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RESULT 2

Q9K5Y6

ID Q9K5
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SEOUENCE 348 AA;
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PROSITE; PS00059; ADH_ZINC; 1.
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MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sa
Fuji F., Hirama C., Nakamura Y., Ogasawara N.,
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180 AWHAVERARFQPGQTALVLGGGPIGLATILALQGHHAGKIVCSEPALIRRQFAKELGAEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002328; ADH_zinc.
InterPro; IPR002085; Adh_zn_family.
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    -!- SIMILARITY: BELONGS TO
FAMILY.

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Bacteria; Firmicutes;
                                                            Horikoshi K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete genome sequence of the alkaliphilic bacterium Bacillus
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                                                                                                                                                                                PHSLTEEKAPIVMGHEFSGQVVEVGDGVTKCEEGDRVVVEPIFAC-----------G
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41; Conservative
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AA; 37516 MW; 28146770BE77FEED CRC64;
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Pred. No. 3.6e-36;
5; Mismatches 134;
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Last annotation updat
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Oxidoreductase; Zinc
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01-MAR-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                      InterPro; IPR002328; ADH_zinc.
InterPro; IPR002085; Adh_zn_family.
InterPro; IPR000205; NAD_binding.
Pfam; PF00107; adh_zinc; 1.
                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of Pseudomonas aeruginosa PAO1, opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                       EMBL; AE004831;
HSSP; P07846; 18
       172
                               181
                                                       113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas.
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I- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYL
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WHAVERARFQPGQTALVLGGGPIGLATILALQGHHAGKIVCSEPALIRRQFAKELGA-EV
                                                               LCMACQSGSPNCCASLSFCGLGGASGGFAEYVVYGEDHMVKLPDSIPDDIGALVEPISVA
                                                                                                                                                                                                                                                                                                                                                                   FAMILY.
                                               TCYYCRHGLYNICENLAFTGLMN-NGAFAEYVNVPANLLYALPAGFPSEAGALIEPLAYG
                                                                                                  PHPLTGLKDQCILGHEFSGEIVRLGNGVTGFAVGQAVAADACQHC---
                                                                                                                MRAAVWHGRHDIRV-EDVPLPAEPPPGWVQIRVHWCGICGSDLHE--YLAGPVFIPVE-A
                                                                                                                                                                                                       136;
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                                                                                                                                                                                                                  Similarity
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uctase; Zinc; Complete
363 AA; 38193 MW;
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16,
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Last annotation update)
                                                                                                                                                                                                 Score 567.5; DB 1
Pred. No. 7.2e-36;
3; Mismatches 141
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3B4DD83ACA1027B8 CRC64;
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                                                                                                                                                                                                   Indels
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Best Local Similarity
Matches 138; Conser
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01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q59696
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Submilted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
SIGNOR: ZINC (BY SINILARITY).
-I- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Huang M., Oppermann F.B., St "Molecular characterization catabolic pathway."; FEMS Microbiol. Lett. 124:14
                                                                                                                                                                                                                                                                                           Oxidoreductase;
SEQUENCE 362 /
                                                                                                                                                                                                                                                                                                               Pfam; PF00107; adh_zinc; 1. PROSITE; PS00059; ADH_ZINC; 1.
                                                                                                                                                                                                                                                                                                                              InterPro; IPR002328; ADH_zinc.
InterPro; IPR002085; Adh_zin_family.
Pfam; PF00107; adh_zinc; 1.
                                                                                                                                                                                                                                                                                                                                                                      EMBL; L35343;
HSSP; P07846;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-PPG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas putida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                       WHAVERARFQPGQTALVLGGGPIGLATILALQGHHAGKIVCSEPALIRRQFAKELGAE-V
                                                                                          LCMACQSGSPNCCASLSFCGLGGASGGFAEYVVYGEDHWVKLPDSIPDDIGALVEPISVA
                                                                                                                                                                                                 MKGLLYYGTNDIRYSETVPEPEIKNPNDVKIKVSYCGICGTDLKEFTYSGGPVFFPKQGT
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FDPSTCDDANAVLKAMVPENEGFHAAFDCSGVPQTFTTSIVATGPSGIAVNVAVWGDHPI
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EELVNNKEHNVKIIVSP 361
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                        MHAVKKAGSLLGQTVVVVGAGTIGLCTIMCAKAAGAAQVIALEMSSARKAKAKEVGATVV
                                                                            TCYYCTHGLYNICERLAFTGLMN-NGAFAELVNVPANLLYRLPQGFPPEAGALIEPLAVG
                                                                                                                                 PHPLTGIQGQCILGHEFCGQIAKLGEGVEGFAVGDPVAADACQHC------G
                                                                                                                                              KDKISGYELPLCPGHEFSGTVVEVGSGVTSVKPGDRVAVEATSHCSDRSRYKDTVAQDLG
::|:|:|||||||:||||:|||
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                                                                                                                                                                                  MRAAVWHGRNDIRV-EQVPLPADPAPGWVQIKVDWCGICGSDLHE--YVAGPVFIPVE-A
                                                                                                                                                                                                                                                                                                                                                                                    L35343; AAB58982.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proteobacteria; gamma
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                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dehydrogenase
                                                                                                                                                                                                                                                                              Zinc.
AA; 38386 MW; 503CD0A58C8BB816 CRC64;
                                                                                                                                                                                                                                                   28.1%;
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on of the Pseudomonas
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Last annotation update)
e (EC 1.1.1.4).
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                                                                                                                                                                                                                                    Score 566.5; DB 2;
Pred. No. 8.5e-36;
5; Mismatches 147;
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                                                                                                                                                                                                                                      27;
                                                                                                                                                                                                                                     Gaps
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ACCORPAGRENCE REPRESENTATION OF REPRESENTATION O
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RX KUDSITE-98044033; PubMed-9384377;
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Chol S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Chol S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Chol S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Chol S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Chistory F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Entian S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Hilbert H., Holsappel S., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kurita K., Lapidus A., Lardinois S., Laber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Mauel C., Medigue C.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Parro V., Pohl T.M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sekiguchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Yoshida K., Yashanoto H., Yamane K., Yashanoto K., Yata K.,
RA Yoshida K., Yashanoto H., Yamane K., Yashanoto K., Yata K.,
RA Yoshida K., Yashanoto H., Yamane K., Yashanoto K., Yata K.,
RA Yoshida K., Yashanoto H., Yamane K., Yashanoto K.,
RA Yashanoto K., Yashanoto H., Yata K.,
RA Yashanoto K., Yashanoto H., 
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01-JAN-1998
01-MAR-2002
                        Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-MARBURG 168;
Kasahara Y., Nakai S.
DNA Res. 0:0-0(1997).
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Bacteria; Firmicutes;
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                                                                                                                                                                                                                                                                  390:249-256(1997).
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ALCOHOL DEHYDROGENASE

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RESULT OCCUPANT OCCUP
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Best Local Similarity
Matches 147; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9CH42;
                 EMBL; AE006323; AAK04995.1; -.
HSSP; P07846; 1SDG.
InterPro; IPR002328; ADH_zinc.
InterPro; IPR002085; Adh_zn_fa
                                                                                                                                                          Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K., Weissenbach J., Ehrlich S.D., Sorokin A., "The complete genome sence of the lactic acid bacterium lactis ssp. lactis IL1403.";
Genome Res. 11:731-753(2001).
-!- COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY (BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcaceae;
NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TIEMBLIFEL 17, C
01-JUN-2001 (TIEMBLIFEL 17, L
01-MAR-2002 (TIEMBLIFEL 20, L
2,3-butanediol dehydrogenase
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                                                                                                                                                                                                                                                                                                        MEDLINE=21235186; PubMed=11337471;
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InterPro; IPR002085; Adh_zn_family.
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                                                                                                                                           SIMILARITY: BELONGS
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; Z99107; CA
; P07846; 1S
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CAB12443.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                  Lactococcus
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    Adh_zn_family
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THE ZINC-CONTAINING ALCOHOL DEHYD
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e (EC 1.1.1.4).
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5E327192D678F8A2 CRC64;
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Best Local
HSSP; PO7846; 1SDG.
HSSP; PO7846; 1SDG.
TIGR; NMB0604; -
InterPro; IPR002328; ADH_zinc.
InterPro; IPR002085; Adh_zn_family.
InterPro; IPR002085; Adh_zinc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000
01-OCT-2000
01-MAR-2002
                                                                                                                                                                                                        Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E. Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vanathevan J.,
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-MC58 / SEROGROUP B;
MEDLINE-20175755; PubMed-10710307;
                                                                                    EMBL; AE002416; AAF41031.1;
                                                                                                                                         Science 287:1809-1815(2000)
                                                                                                                                                        "Complete genome sequence of Neisseria meningitidis
MC58.";
                                                                                                                                                                                  Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter
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                                                                                                                                                                                                                                                                                                                                                               Neisseria meningitidis (serogroup
Bacteria; Proteobacteria; beta suk
                                                                                                                                                                                                                                                                                                                                                                                                         Alcohol
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                                                                                                                -!- SIMILARITY:
                                                                                                                            -! - COFACTOR:
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3; Mismatches
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Pred. No. 1.
                                                                                                               R ITS ACTIVITY (BY ZINC-CONTAINING AI
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D53348B51D8030DB CRC64;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O9JVJ8 PRELIMINA...,
O9JVJ8;
O1-CT-2000 (TrEMBLrel. 15, Creation of the control o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00059; ADH_ZINC; 1: Oxidoreductase; Zinc; Complete SEQUENCE 354 AA; 37920 MW;
PROSITE; PS00059; ADH_ZINC; 1.
Oxidoreductase; Zinc; Complete
SEQUENCE 354 AA; 77000
                                                                              EMBL; AL162754; CAB84091.1; -.
HSSP; P07846; 1SDG.
InterPro; IPR002328; ADH_Zinc.
InterPro; IPR002085; Adh_zn_family.
Pfam; PF00107; adh_zinc; 1.
                                                                                                                                                                                                                                                                                                           Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T. Bavies R.M., Davies P., Deviln K., Feltwell T., Hamilin N., Ho Jagels K., Leather S., Moule S., Wungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; Whitehead S., Spratt B.G., Barrell B.G.; Barrain of Neisseria
                                                                                                                                                                                                                      meningitidis 22491.";
Nature 404:502-506(2000).
-!- COFACTOR: REQUIRES ZI
-!- SIMILARITY: BELONGS T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-22491 / SEROGROUP A / SEROTYPE 4A; MEDLINE-20222556; PubMed-10761919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-22491 / SEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria;
NCBI_TaxID=65699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis (serogroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NMA0808
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Last annotation updat
ol dehydrogenase (EC )
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Pred. No. 1.6e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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2EF4DBACF877C35E
                proteome.
CEE7B4CFE0C38990 CRC64;
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Best Local 9
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                     InterPro; IPR002328; ADH_zinc.
InterPro; IPR002085; Adh_zn_family.
InterPro; IPR002040; Tachykinin.
Pfam; PF00107; adh_zinc; 1.
PROSITE; PS00059; ADH_ZINC; 1.
PROSITE; PS00059; ADH_ZINC; 1.
PROSITE; PS00267; TACHYKININ; UNKNOWN_1.
                                                                                                                                                                      EMBL; AE004826; AAG07484.1; HSSP; P07846; 1SDG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probable alcohol PA4097.
  Oxidoreductase; SEQUENCE 352 /
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                   Zinc;
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    complete 37603 MW;
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                Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.;
                                                                                                 MEDLINE=21608551; PubMed=11743194;
                                                                                                                                     Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 21nc-binding dehydrogenase.
                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                       ATU4740 OR AGR_L_281.
Agrobacterium tumefaciens
                                                                                                                                                                                           Wester E.W.
                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
Rhizobiaceae; Rhizobium.
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096496;
01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-MAR-2002 (TrEMBLrel. 20,
                                             InterPro; IPR002328; ADH_zinc.
InterPro; IPR002085; Adh_zn fa
InterPro; IPR001327; FAD_pyr_r
InterPro; IPR001377; FAD_pyr_r
Pfam; PF00107; Adh_zinc; 1.
PRINTS; PR00368; FADPNR.
                                                                                                                                                                    -i- COFACTOR: FAD (BY SIMILARITY).
-i- COFACTOR: ZINC (BY SIMILARITY).
EMBL; AF067126; AAD02817.1; -
HSSP; P07846; 1SDG.
                                                                                                                                                                                                                                                                                        differences between whitefly ketose reductase dehydrogenases/reductases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bemisia argentifolii (silverleaf whitefly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; insecta;
Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;
Aleyrodiformes; Aleyrodoidea; Aleyrodidae; Aleyrodinae; Bemisia
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=99212467;
                    PROSITE; PS00059; ADH_ZINC;
                                                                                                                                                                                                                                                                                                                                        MEDLINE=99212467; PubMed=10196734; Wolfe G.R., Smith C.A., Hendrix D.L., "Molecular basis for thermoprotection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=77855;
                                                                                                                                                                                                                                                                      Insect Biochem. Mol. Biol.
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Science 294:233-2328(2001).
EMBL; AE009402; AAL45534.1; ALT_
EMBL; AE008211; AAK88710.1; -
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                           Salvucci M. in Bemisia:
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Query Match
Best Local Similarity
Matches 112; Conser
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021702;
01-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-MAR-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                   investigating biology.";
Science 282:2012-2018(1998).
-- COFACTOR: ZINC (BY SIMILARITY).
EMBL; 270782; CAA94841.1; --
HSSP, P07846; ISDG.
                                                                                                                                                                                               InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wilkinson
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                                                                                     Oxidoreductase; Zi
                                                                                                                                                                                                                                                                                                                                                                           none;
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-6239;
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                                                                                                                                                                                                                                                                                                                                                      Genome sequence of the nematode C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE FROM N.A.
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                                                                                                                                            PF00107338; ADH_zinc.
Pro; IPR002085; Adh_zn_family.
Pro; IPR00205; NAD_binding.
PF00107; adh_zinc. 1
                                                                                                                            00107; adh_zinc; 1.
PS00059; ADH_ZINC; 1.
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AA: 37323 MW;
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62;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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Pred. No. 4.8e-24;
Score 386.5; DB 5;
Pred. No. 6.9e-22;
2; Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56360D3D2EDA6D26 CRC64;
                                                                                       AE71536D4B1344B0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                     "Xylose utilisation: Cloning and characterisation of dehydrogenase from Galactocandida mastotermitis."; Submitted (JUN-1998) to the EmbLyGenBank/DDBJ databas: -- COFACTOR: ZINC (BY SIMILARITY).

EMBL; AF072541; AAC24597.1; -- HSSP; PO7846; ISDG.
InterPro; IPR002328; ADH_zinc.
InterPro; IPR002025; NAD_binding.
                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last.annotation update)
xylitol dehydrogenase (EC 1.1.1.9).
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Eukaryota; Fungi;
                                                                                                                                                                                                                                                                                                                                                Oxidoreductase; Zinc.
SEQUENCE 353 AA; 37382 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomycetales;
NCBI_TaxID=78167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XDH.
                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                               11 DIRYSETYPEPEIKNPNDVKIKVSYCGICGTDLKEFTYSGGPVFFPKQGTKDKISGYELP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGRYNLCPEMRFFATPPVHGTLSRFVVHDADFCFKLPDNLSFEDGALIEPLSVAIHACRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---PMIVGHETSGIVSEVGNEVKHLKVGDRIAMEPGLPCK----
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                                                                                                                                                KGFKQLIEHKENNVKILV
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                                                                                  LCPGHEFSGTVVEVGSGVTSVKPGDRVAVEATSHCSDRSRYKDTVAQDLGLCMACQSGSP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EAFKR--TQKADVIKVFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIGFMPMSLTYQEKYATGSMCYTVKDFQEVVKALEDGLISLDKARKMITGKVHLK-DGVE
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                                                   MVLGHESSGVVLEVGSEVKSLKVGDRVAMEPGVPSRHSDEYK---
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  NCCASLSFCGLGGASGGFAEYVVYGEDHMVKLPDSIPDDIGALVEPISVAWHAVERARFO
                                                                                                                                                                                                                                                                          Similarity
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PS00059; ADH_ZINC; 1.
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                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ascomycota; mitosporic
                                                                                                                                                                                                                                                19.2%; Score 386.5; DB 3 30.6%; Pred. No. 7.1e-22; tive 48; Mismatches 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                     9BA7F10CE9F6E687 CRC64;
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                                                                                                                                                                                                                                                                                                    DB 3;
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xylitol
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                                                        SGRY
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                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

SETRAIN-MSB8 / DSM 3109;

MEDLINE=99287316; PubMed=10360571;

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Nelson K.E., Clayton R.A., Gill S.R., Nelson W.C., Ketchum K.A.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria from the state of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999
01-NOV-1999
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00059; ADH_ZINC; 1.
Oxidoreductase; Zinc; Complete
SEQUENCE 395 AA; 43317 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TM0412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGR; TM0412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alcohol dehydrogenase, zinc-containing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9WYP3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9WYP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermotoga maritima
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                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY (BY SIMILARITY) SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAMILY.
                                                                                                                   GTKDKISGYELPLCPGHEFSGTVVEVGSGVTSVKP-----GDRVAVEATSHCSDRSRYK 112 :: |: | | | |
                                                                                                                                                                                 LTWLGSKVWRYPEVRVEEVPEPRIEKPTEIIIKVKACGICGSDVHMAQTDEEGYILYP--
                                             DTVAQDLGLCMACQSGSPNCCASLSFCGLGGASGGFAEYV----
                                                                                        ----GLTGF---PVTLGHEFSGVVVEAGPEAINRRTNKRFEIGEPVCAEEMLWC
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Pro; IPR002085; Adh_zn_family.
Pro; IPR000205; NAD_binding.
PF00107; adh_zinc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATLIGKELTVKGSFRYGYGDYPLAVSLLASGKVNV---KKLITHEVKFEDAAEAFQLVRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESAAKVVAA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NICPHNAFAATPPYDGTLCKYYILPEDFCVKLPEHVSLEEGALVEPLSVAVHSSKLGNIK 169
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                                                                                                                                                                                                                                                                                      109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AE001720; AAD35497.1;
                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR002328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermotogae;
-GHCRPCAEGFPNHCENLNELGF-NVDGAFAEYVKVDAKYAWSLRELEGVYEGD
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                      18.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADH_zinc.
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12,
20,
                                                                                                                                                                                                                                                                                 37;
                                                                                                                                                                                                                                                                            Score 370; DB 16;
Pred. No. 1.6e-20;
7; Mismatches 111;
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                       proteome.
29D2A19F00946397 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       395
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                                                                                                                                                                                                                                                                                                                            Length 395;
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                                           ----VYGED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria from
                                                                                                                                                                                                                                                                               64;
                                                                                                                                                                                                                                                                            Gaps
                                                                                        131
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RX MEDLINE-98044033; PubMed-9384377;
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Bilgnell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Coddani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Gims S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Giseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Giseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Fohl T.M., Portetelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Viatai A., Wandmutt R., Wedler E., Wedler H., Weitzenegger T.,
Whiters P., Wajat A., Yanamoto H., Yanane K., Yasumoto K., Yata K.,
RA The complete genome sequence of the gram-positive bacterium Bacillus
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Kunst F., Ogasawara N., Yoshikawa H., Danchin Submitted (NOV-1997) to the EMBL/GenBank/DDBJ -!- COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY (
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InterPro; IPR002085; Adh_zn_family.
Pfam; PF00107; Adh_zinc; 1.
PROSITE; PS000059; ADH_ZINC; 1.
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                                                                 319 HAFQFIKEHPDQVRKAVIT 337
                                                                                                                                       267 QISOLPITKKEVTITGSRLQT-NQFPKVVELLNGG-----RLMHNGLVTHTFSVDDVH 318
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SUMMARIES

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Haselbeck R, Yamamoto RT,

Ohlsen KL, Zyskind JW, Wall D, xu HH;

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Carr GJ;

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 Lactococcus
                                      16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part
                                                                      ABB54213;
                                                                                                       ABB54213 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                              345
                                                                                                                                                                                                                                                                                                                                                                                                       172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pneumoniae, Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Seq ID No 11979; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                 289
                                                                                                                                                                                                                                                                                                                                                                     240
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                                                                                                                                                                                                                                                                                                                                                                                                                                        181
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                                                                                                                                                                                                                                                                                                                                                          FDPSTCDDANAVLKAMVPENEGFHAAFDCSGVPQTFTTSIVATGPSGIAVNVAVWGDHPI
                                                                                                                                                                                                                                                                                                                                                                                                                         WHAVERAREQPGQTALVLGGGPIGLATILALQGHHAGKIVCSEPALIRRQFAKELGA-EV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LCMACQSGSPNCCASLSFCGLGGASGGFAEYVVYGEDHMVKLPDSIPDDIGALVEPISVA
                                                                                                                                                                                                              KQLIEHKENNVKILVTP 376
                                                                                                                                                                                                                                                          EFNFFELVSTEKQLLGALAYN-GEFADVIAFIADGRLDI---APLVTGRIGLEEIVERGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCYYCRHGLYNICENLAFTGLMN-NGAFAEYVNVPANLLYALPAGFPSEAGALIEPLAVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MRAAVWHGRHDIRV-EDVPLPAEPPPGWVQIRVHWCGICGSDLHE--YLAGPVFIPVE-A
                                                                                                                                                                                            EELVNNKEHNVKIIVSP 361
                                                                                                                                                                                                                                                                                          GFMPMSLTYQEKYATGSMCYTVKDFQEVVKALEDGLISLDKARKMITGKVHLKDGVEKGF
                                                                                                                                                                                                                                                                                                                           LDPSRC-DALGEIRALT-GGLGADVSFECIGNKHTAKLAIDAIRKAGKCVLVGIF-EEPS
                                                                                                                                                                                                                                                                                                                                                                                                MHAVKKAGSLLGQNVVVVVGAGTIGLSTIMCARAAGAAQVIALEMSSARKAKALEVGASQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHPLTGLKDQCILGHEFSGEIVRLGNGVTGFAVGQAVAADACQHC-------G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MKGLLYYGTNDIRYSETVPEPEIKNPNDVKIKVSYCGICGTDLKEFTYSGGPVFFPKQGT
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lactis protein
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                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus, Salmonella typhi, Klebsiella Staphylococcus aureus, Salmonella typhi, Klebsiella omonas aeruginosa and Enterococcus faecalis. The useful for the identification of potential new targets
                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.2%;
 butB.
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                                                                                                       370
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Pred. No. 7.5e-48;
3; Mismatches 141;
                                                                                                     A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                           production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent w0200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the imposition are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; SEQ
 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INRG ) INRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biosynthesis; biodegradation;
                                                                                                                                                                                                                                                                         71
                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                               61 KDKISGYELPLCPGHEFSGTVVEVGSGVTSVKPGDRVAVE--ATSHCSDRSRYKDTVAQD
                                                                                                                                                                                                                                                                                                                           15 MRAARFYDRGDIRIDE-INEPIVK-AGQVGIDVAWCGICGTDLHEFL--DGPIFCPSAEH
                                                                                                                                                                                                                                                                                                                                           VAWHAVERARFQPGQTALVLGGGPIGL--ATILALQGHHAGKIVCSEPALIRRQFAKELG
LDDLIDKGFDTLIHHNETAVKILVSP
                         LKDGVEKGFKQLIEHKENNVKILVTP
                                                                             VAVWGDHPIGFMPMSLTYQEKYATGSMCYTVKDFQEVVKALEDGLISLDKARKMITGKVH
                                                   VAIWG-KPASVDMAKLVIKEANLLGTIAYN-NTHPKTIDLVSTGKIKLD---QFITAKIG
                                                                                                           AQVADYFFNPIEDD
                                                                                                                                  AEV----FDPSTCDDANAVLKAMVPE--NEGFHAAFDCSGVPQTFTTSIVATGPSGIAVN
                                                                                                                                                              VGYHAVERANLSEKSTVLVVGAGPIGLLTAAVAKAQGH---TVIISEPSGLRRKKAQE--
                                                                                                                                                                                                                                           LGLCMACQSGSPNCCASLSFCGLGGASGGFAEYVVYGEDHMVKLPDSIPDDIGALVEPIS
                                                                                                                                                                                                                                                                       PNPITGEVPPVTLGHEMSGVVNFIGEGVSGLKVGDHVVVEPYIVPEGTDTS------
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                                                                                                                                                                                                                                                                                                                                                                                   144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cleotide sequence useful in and related species -
                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       370 AA;
                                                                                                                                                                                                                  ETGHYNLSEGSNFIGLGGNGGGLAEKISVDERWVHKIPDNLPLDEAALIEPLS
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ID No 915; 2504pp; .French.
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                                                                                                        ----IQAKVHEINEKGVDAAFECTSVQPGFDACLDAIRMGGTVVI
                                                                                                                                                                                                                                                                                                                                                                                               26.8%;
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                                                                                                                                                                                                                                                                                                                                                                                53;
                                                                                                                                                                                                                                                                                                                                                                                Score 538.5; DB:
Pred. No. 6.2e-45;
3; Mismatches 14:
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365
                           376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identification or Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ehrlich
                                                                                                                                                                                                                                                                                                                                                                                  144;
                                                                                                                                                                                                                                                                                                                                                                                                           23;
                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                                                                                                                                           370;
                                                                                                                                                                                                                                                                                                                                                                                45;
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of

RESULT 3 AAE21046

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Baughn
Gandhi
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18-AUG-2000;
24-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acquired immunodeficiency syndrome; AIDS; glomerulonephritis; anorectic; diabetes; atherosclerosis; adult respiratory distress syndrome; anaemia; Grave's disease; thyroiditis; Crohn's disease; infection; anticoagulant; systemic lupus erythematcsus; cirrhosis; psoriasis; epileps; gastritis; cataract; hypopitultarism; cancer; rheumatod arthitis; conjunctivitis; cataract; hypopitultarism; cancer; rheumatod arthitis; conjunctivitis; cystic fibrosis; peptic ulcer; Wilson's disease; hepatitis; antithyroid; allergy; diarrhoea; thrombosis; obesity; immunostimulant; tranquillizer; infertility; vulnerary; anticonvulsant; gynaecological; laxative; goitre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pancreatic;
                                                                                                                                                                                                                 Claim 48; Page 149-150;
                                                                                                                                                                                                                                               New human drug metabolizing enzyme polypeptide and polynucleotide useful for diagnosing, treating and preventing cell proliferative, autoimmune/inflammatory, endocrine, eye, metabolic and gastrointes
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                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                  31-AUG-2000;
13-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                 (INCY-)
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                                                                                                                                                                                                                                                                                                         2002-206331/26
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                                                                                                                                                                                                                                                                                                                      Lu Y, FILL K, T Thangavelu K, T Than Yang J, Yao M
                                                                                                                                                                                                                                                                                                                                 BA,
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                                                                                                                                                                                                                                                                                               AAD33483
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Griffin JA, Hafalia AJA, Khan FA, Lal
Y, Patterson C, Ramkumar J, Ring HZ,
hangavelu K, Thornton M, Tribouley CM,
Yang J, Yao MG, Yue H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      metabolising enzyme; cell proliferative disorder; metabolic; inflammatory; developmental; gastrointestinal; hypergonadal; endocrine; eye; dermatitis; Addison's disease; antilipaemic;
                                                                                                                                                                                                                                                                                                                                                                                                                     ; 2000US-224728P.
; 2000US-226440P.
; 2000US-228067P.
; 2000US-230063P.
; 2000US-232244P.
; 2000US-234269P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry
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                                                                                                                                                                                                                                                                                                                                                                                                  GENOMICS
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                                                                                                                                                                                                                                                                                                                                                                                                 INC.
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mellitus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enzyme
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'A, Lal |
 disorders
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Walia NK;
                                                                                                                                                                                                                                                 gastrointestinal
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RESULT 4
ABP38529
ID ABP38529
ID ABP3
XX ABP3
XX Stap
DE Stap
XX Stap

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                                                                                                                                                          14-AUG-1997;
08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus
                                                                                                     (GENO-)
                                                                                                                                                                                                                                  13-AUG-1998;
                                                                                                                                                                                                                                                                                     30-APR-2002.
                                                                                                                                                                                                                                                                                                                                        US6380370-B1
                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                          antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus
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Pred. No. 4.4e-43;
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N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                 27-SEP-2001
                                                                                       WO200170955-A2
                                                                                                                                                                                                    Antisense; prokaryotic cellular antibiotic; antibacterial; drug
                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa cellular
                                                                                                                                                                                                                                                                                                                                                     14-FEB-2002
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                                                                                                                                             Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU36382 standard; Protein; 352
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Pred. No. 2.9e-40;
                                                                                                                                                                                                    proliferation protein design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prokaryotic cellular proliferation, their use in identifying the components, their use in the discovery of novel antiblotics, the essential components themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella components are services and Enterococcus faecalis. The service invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an cessential prokaryotic cellular proliferation protein.

Componential prokaryotic cellular proliferation for the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity Matches 127; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to antisense inhibitors of genes essential prokaryotic cellular proliferation, their use in identifying the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example
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RLDAFDLVNRELRLLGSVGY -- RDAYPELIALLADGRLDLARA -- - VTRSVPLEQAVEHG
                                                                                                                                                                                                                                                                                                                                                 ECRYCREGRYNLCESMGFIGLMG-DGGFAERARVPAYMLHRLPDAVGFRQAAVLEPAAVA
                                                                                                                                                                                                                                                                                                                                                                                                           LCMACQSGSPNCCASLSFCGLGGASGGFAEYVVYGEDHMVKLPDSIPDDIGALVEPISVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDKISGYELPLCPGHEFSGTVVEVGSGVTSVKPGDRVAVEATSHCSDRSRYKDTVAQDLG
                                                   GFMPMSLTYQEKYATGSMCYTVKD-FQEVVKALEDGLISLDKARKMITGKVHLKDGVEKG
                                                                                                                                                                                                                                                                                    WHAVERARFQPGQTALVLGGGPIGLATILALQGHHAGKIVCSEPALIRRQFAKELGA-EV
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AHPLSGCRAPLTLGHEFCGVVAALGPGVEGPRIGDRVAVEPEYRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKALRWHAARDLRLSEL - - ERQAPRPGEVELEVAYCGICGSDLHE - - YQSGPHSIP - QAE
                                                                                                             LDARDGDTA-
                                                                                                                                                                    FDPSTCDDANAVLKAMVPENEGFHAAFDCSGVPQTFTTSIVATGPSGIAVNVAVWGDHPI
                                                                                                                                                                                                                                 LHALRRSSLAPGQRCAVFGLGPIGLLLVMLARLRGIEDIAAVDVSPERLALAGEFGASRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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2000US-257931P.
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2000US-242578P.
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Xu HH;
                                                                                                                ARLREGGALDCAFEAAGSQASLDAALASLRKGGELVLVSLMGE--V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 455.5; DB 2
Pred. No. 1.2e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wall
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 352;
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FEALLRDK-SQLKVLVNPN 346 FKQLIEHKENNVKILVTPN

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RESULT 6
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                                                                                                                        Matches
                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                              (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
(I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to
                                                                                                                                                                                                                                            AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus epidermidis SR1 strain; infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S. epidermidis open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG81823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG81823 standard; Protein; 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 18; Page 228; 2188pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-316495/33.
N-PSDB; AAH52673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kimmerly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-NOV-2000; 2000WO-US30782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccination;
                                                                                                                                                                                                                             no sequences are present for SEQ ID NO:4455 to 4464.
                    61
                                                     ш
KDKISGYELPLCPGHEFSGTVVEVGSGVTSVKPGDRVAVEATSHCSDRSRYKDTVAQDLG
                                                   MKAAVWYGQKDVRVEDR--EPKAIKDNEVQVKVSWAGICGTDLHE--YLEGPIFI-STDQ
                                                                         MKGLLYYGTNDIRYSETVPEPEIKNPNDVKIKVSYCGICGTDLKEFTYSGGPVFFPKQGT
                                                                                                                        111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to AAH53970 represent nucleic acids (I) encoding
                                                                                                                                                                                            291 AA;
                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             endocarditis.
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                                                                                                                                         36.48;
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                                                                                                                      Score 417.5; DB 22; Pred. No. 5.4e-33; Pred. No. 5.4e-33; No. Mismatches 123;
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                                                                                                                        Indels
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                                                                                                                                                           291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptides
                                                                                                                        29;
                                                                                                                      Gaps
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ETVPEPEIKNPNDVKIKVSYCGICGTDLKEFTYSGGPVFFPKQGTKDKISGYEL--PLCP 73

Query Match Best Local Sim Matches 111;

Similarity

Conservative

56;

Mismatches 160; .8e-27

Indels

39;

Gaps

11;

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RESULT 7
AAR56479
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                                         Sequence
                                                              This sequence (AAR56479) is that of sorbitol dehydrogenase. The presence of eleven amino acids of the sorbitol dehydrogenase from its N-terminal in a fusion polypeptide results in several fold higher levels of expression of the fused polypeptides as compared to the unfused polypeptide. The DNA encoding the enzyme is shown in AAQ66579, it is useful for its regulatory elements. These can be used in yeast hosts for the production of heterologous proteins, eg. superoxide dismutase or the hepatitis delta antigen.
                                                                                                                                                                                                  Claim 27; Page 31-34; 60pp; English.
                                                                                                                                                                                                                          Purified yeast sorbitol dehydrogenase - used for isolating regulatory sequences for use in expressing heterologous polypeptide(s) in yeast
                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                   WPI; 1994-249120/30
                                                                                                                                                                                                                                                                                                                              Sarthy AV, Schopp CW;
                                                                                                                                                                                                                                                                                                                                                                                      30-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sorbitol dehydrogenase; yeast regulatory sequence; assay reagent; heterologous protein expression; superoxide dismutase; antibody; hepatitis delta antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sorbitol dehydrogenase from Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR56479;
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                                                                                                                                                                                                                                                                                                                                                                                                                  22-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                         (ABBO ) ABBOTT LAB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WHAVERARFQPGQTALVLGGGPIGLATILALQGHHAGKIVCSEPALIRRQFAKELGA-EV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GFMPM 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YNSGNYDPYQTYYE---HTDNGYDYSFEVAGYGITLQQSIEVTRPRGTAVIVSIFG-HPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VQAVKEGELLFGDTVAVFGAGPIGLLTIVAAKAAGASKIFVFDLSEERLAKAKSVGATHV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDPLLGQTAPVTLGHEFSGVIENVGKDVSRFKKGDRVVVNPT--VSKREKPENVDLYD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FDPSTCDDANAVLKAMVPENEGFHAAFDCSGVPQTFTTSIVATGPSGIAVNVAVWGDHPI 299
                                                                                                                                                                                                                                                                                      AAQ66579.
                                         357 AA;
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17.9%;
30.3%;
Score 360.5;
Pred. No. 3.8
             DB 15;
             Length
              357;
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Chakraborty T, pom...
Chakraborty T, Baguero F
Perez-Diaz J, Baguero F
Perez-De Pablos P
                                                                                                                                                                                                                    Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux I Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossari Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-García P, Tierrez-Martinez A, Amend J, Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L, Perez-Diaz J, Baquero F, García Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J,
The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments it are useful for selecting probes and primers for detecting genes in monocytogenes and related organisms, and for studying genetic
                                                                                                            Genomic sequence for Listeria monocytogenes, useful e.g. for and prevention of Listeria and related bacterial infections, related polypeptides
                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibacterial; gene therapy; vaccine; biosynthesis; vitamin B12; bacterial infection; disease.
                                                                                    Claim
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                                                                               ID No 602; 192pp; French
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Best Local
                                                                 WO200153306-A2
                                                                                                 Clostridium difficile
                                                                                                                                               Pive-carbon sugar; aldo-sugar; keto-sugar; sugar alcohol; fer
pentose phosphate pathway; xylitol; D-arabitol; D-arabinose;
ribitol; D-ribose; D-ribulose; D-xylose; D-xylulose; microbia
arabitol phosphate dehydrogenase; APDH; xylitol phosphate deh
                                                                                                                                                                                                                                   Clostridium
                                                                                                                                                                                                                                                                                                    AAE05988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, antibodies, identification of L. monocytogenes and related organisms.
                                                                                                                                                                                                                                                                    24-SEP-2001
                                                                                                                                                                                                                                                                                                                                 AAE05988 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specification,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 KDKISGYELPLCPGHEFSGTVVEVGSGVTSVKPGDRVAVEATSHCSDRSRYKDTVAQDLG
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                                                                                                                                                                                                                                                                                                                                                                                                                   RLSLAEGPEV-FERIYERNEFFGKVLFFP 347
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                                                                                                                                                                                                                                difficile homologue protein
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Pred. No. 5.7e-27;
""ematches 159;
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26-JUL-2001

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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to the methods for manufacturing five-carbon aldo- and keto-sugars and sugar alcohols by fermentation in recombinant hosts. The recombinant hosts of the invention have been engineered to enhance the production of the pentose phosphate pathway intermediates, or the production of one or more of xylitol, D-arabicol, D-arabinose, D-lyxose, ribitol, D-ribose, D-ribuse, D-xylose and/or D-xylulose, D-lyxose, ribitol, D-ribose, D-ribused in a microbial host cell to produce recombinant arabitol. Xylitol phosphate dehydrogenase (XPDH) and arabitol phosphate dehydrogenase are used in a microbial host cell to produce recombinant xylitol. The present sequence, is Clostridium difficile homologue protein which is homologous to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated polynucleotide, used to transform bacterial or yeast hosts which can then be used in the production of sugars and sugar alcohols, encodes xylitol phosphate dehydrogenase -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 16; Page 199-200;
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              26-MAR-2002
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                                                                                                                                                                                                                                                                                   207
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                                                                                                                                                                                     ARKMITGKVHLKDG---VEKGFKQ 361
                                                                                                                                                                                                                                                  VAVWGDHPIGFMPMSLTYQEKYATGSMCYTVK----DFQEVVKALEDGLISLDK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KQGTKDKISGYELPLCPGHEFSGTVVEVGSGVTSVKPGDRVAVEATSHCSDRSRYKDTVA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MKGLLYYGTNDIRYSETVPEPEIKNPNDVKIKVSYCGICGTDLKEFTYSG----GPVFFP 56
                                                                                                                                                       VEKLYTHRINLEEAPAYFEKVYKR
                                                                                                                                                                                                                                                                                                                                               VCIAGHGLFRSEAKVGDTVVVLGTGPIGLFSIQWAKIFGSTKIIAVDVFDEKLDLAKELG
                                                                                                                                                                                                                                                                                                                                                                         ISVAWHAVERAREOPGOTALVLGGGPIGLATILALOGHHAGKIVCSEPALIRROFAKELG
                                                                                                                                                                                                                                                                                                                                                                                                                                           QDLGLCMACQSGSPNCCASLSFCGLGGASGGFAEYVVYGEDHMVKLPDSIPDDIGALVEP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKSVRFYGIRDTRV-EDVDVPKILEKDDVIIKVKVAGICGSDISKYSKTGPHMVGEIL--
                                                                                                                                                                                                                                                                                  ADI-----C--INAKEKNIVEEIKRLTDGDGADIVIESAGTPLTCGQVLLLAKKGGTVLY 259
                                                                                                                                                                                                                                                                                                               AEVFDPSTCDDANAVLKAMVPE-----NEGFHAAFDCSGVPQTFTTSIVATGPSGIAVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GHEFSGEVAQVGKEVRSFKIGDRVAVCPAMPCFE-----
                                                                                                                                                                                                                     AGV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     al Similarity
111; Conser
                                                                                                                                                                                                                                                                                                                                                                                                              -CDECKKGLYSRCNNVAIIGNKELGGCFAEYTKVKERNLIKIPDEISYETAAALEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                350 AA;
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                                                                                                                                                                                                                     PYGDVALTREQFEKIVRSEL--TVKGTWFGNSFPFPGKEWSAGLYHMQKGDMN
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Kolvuranta K, Londesborough
Plazanet-Menut C, Deutscher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0488581
              (first entry)
                                                                           Protein;
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Pred. No. 8.2e-27;
9; Mismatches 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
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ugh J, 🗜
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Aristidou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 350;
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RESULT 11
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Best Local S
Matches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and. cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLI6176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila; developmental biology;
pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions
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11-JUL-2000;
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                                                                                                    222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                      YGTNDIRYSETVPEPEIKNPNDVKIKVSYCGICGTDLKEFTYSGGPVFFPKQGTKDKISG 66
:| |:| | | | | | |: ::| :: ||||:|: :: ||
HGIEDLRL-EQRPIPEIAD-DEVLLAMDSVGICGSDVHYLAHG------RIGD 55
                                                                                                                                                                                                                                                                               FVLTKPMIIGHEAAGVVAKLGKKVTTLKVGDRVAIEPGVPC----
                                                                                                                                                             RRAGVGLGSKVLILGAGPIGLVTLLAAQAMGASEILITDLVQQRLDVAKELGATHTLLLQ
                                                                                                                                                                                                                     CKQGRYNLCADMVFCATPPYDGNLTRYYKHAADFCFKLPDHVSMEEGALLEPLSVGVHAC 161
                                                                                                                                                                                                                                        CQSGSPNCCASLSFCGLGGASGGFAEYVVYGEDHMVKLPDSIPDDIGALVEPISVAWHAV 184
                                                                                                                                                                                                                                                                                                         YEL--PLCPGHEFSGTVVEVGSGVTSVKPGDRVAVEATSHCSDRSRYKDTVAQDLGLCMA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-656860/75.
DB; ABL04912.
                                                                                                                              FDPSTCDDANAVLKAM--VPENEGFHAAFDCSGVPQTFTTSIVATGPSGIAVNVAV
                                                                                                    RDQSAEETVKVVHQTMSEVPDK----
                                                                                                                                                                                       ERARFQPGQTALVLGGGPIGLATILALQGHHAGKIVCSEPALIRRQFAKELGAE----V 239
                                                                                                                                                                                                                                                                                                                                                                                                  98;
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کار
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2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                40;
                                                                                                                                                                                                                                                                                                                                                                                                Score 355.5; DB 22;
Pred. No. 1.2e-26;
40; Mismatches 115;
                                                                                                    --SIDCCGAESSARLAIFATRSGGVVVVVGM
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Best Local S
Matches 108
                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to the methods for manufacturing five-carbon aldo- and keto-sugars and sugar alcohols by fermentation in recombinant hosts. The recombinant hosts of the invention have been engineered to enhance the production of the pentose phosphate pathway intermediates, or the production of one or more of xylitol, D-arabitol, D-arabinose, D-lyxose, ribitol, D-ribose, D-ribulose, D-xylose and/or D-xylulose. Arabitol phosphate dehydrogenase (APDH) is used in a microbial host cell to produce recombinant arabitol. Xylitol phosphate dehydrogenase (XPDH) and arabitol phosphate dehydrogenase are used in a microbial host cell to produce recombinant xylitol. The present sequence is Bacillus halodurans sorbitol dehydrogenase protein which is homologous to Lactobacillus rhammosus XPDH protein.
                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 14; Page 197-198; 205pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated polynucleotide, used to transform I which can then be used in the production of encodes xylitol phosphate dehydrogenase -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
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Penttilae M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Five-carbon sugar; aldo-sugar; keto-sugar; sugar alcohol; fermentation; pentose phosphate pathway; xylitol; D-arabitol; D-arabinose; D-lyxose; ribitol; D-ribose; D-ribulose; D-xylose; D-xylulose; microbial host; arabitol phosphate dehydrogenase; APDH; xylitol phosphate dehydrogenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Miasnikov A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (XYRO-) XYROFIN OY.
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      210
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                              241 DPSTCDDANAVLKAMVPENEGFHAAFDCSGVPQTFTTSIVATGPSGIAVNVAVWGDHPIG
                                                                                                                                                           121
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                                                                                                                                                   LCMACQSGSPNCCASLSFCGLGGASGGFAEYVYYGEDHMYKLPDSIPDDIGALVEPISVA 180
                                                                                                                                                                                                          MKGLLYYGTNDIRYSETVPEPEIKNPNDVKIKVSYCGICGTDLKEFTYSGGPVFFPKQGT
ISSLQRPAHKQILEYT-NGIGVDVAVESAGTPSTSAQVFALPKKGGEVVFLGI----PYA
                                                                                          WHAVERARFQPGQTALVLGGGPIGLATILALQGHHAGKIVCSEPALIRRQFAKELGAEVF
                                                                                                                                                                                        -KKLGPYVPGMTFGHEFAGEVVKIGRSVTGFSIGDRVAACPTYTC-
                                                                                                                                                                                                                                                    MKALNLYGIQDLRFEET-PAPSIEHDDDIIIKVKAVGICGSDLSRY------
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                                                             AHGFYRTNIKPGASVAIMGVGSIGLLAVQWAKIFGATTVFAIDIDEQKLNVANQLGADVL
                                                                                                                          QCRYCQLGEPTRCERLSVIG-ARHPGAYAEYVKLPAKHVIPLPNVVNYDEAALIEPASVV
                                                                                                                                                                                                                                                                                                                 108;
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Koivuranta K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dehydrogenase
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                                                                                                                                                                                                                                                                                                                            17.5%;
27.6%;
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                                                                                                                                                                                                                                                                                                         Score 352.5; DB 22,
Pred. No. 2.3e-26;
""ematches 176;
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Aristidou
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RESULT 12
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AAB58718
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Matches 106
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                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                      specification, but was writered in quences at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 2946; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic a genes from Drosophila interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Venter JC,
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11-JUL-2000;
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Pred. No. 2.4e
53; Mismatches
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                                                                              studies facilitating better understanding of carbohydrate metabolism and function in plants, for providing genetic tools for the manipulation of the sorbitol biosynthetic pathway, and for providing means to control
                                                                                                                                                                  The sequences given in AAH43311-17 encode enzymes which were used for comparison in the isolation of proteins having aldehyde reductase activity. The isolated aldehyde reductase sequences were identified based on Clustal alignment method. The aldehyde reductase cDNA, operatively linked to a plant specific promoter, is useful for altering the level of expression of aldehyde reductase in a transformed host cell. The aldehyde reductase is also useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid sequence encoding a polypeptide having aldehyde activity, useful for transforming plants with altered levels expression of sorbitol biosynthetic enzymes -
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lism; sorbitol biosynthesis; carbon partitioning;
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Sequence

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Claim 6;

SEQ ID No

2215; 192pp;

French.

related polypeptides

polymorphisms encoded by the

monocytogenes it are useful

invention relates to the genome sequence of Listeria es EGD e (see ABA03041). The genome sequence and fragments ul for selecting probes and primers for detecting genes in es and related organisms, and for studying genetic es and other genomes. The present sequence is a protein the control of the present sequence.

F of

Genomic sequence for Listeria monocytogenes, useful e.g. for and prevention of Listeria and related bacterial infections,

treatment and

HPI; Rose

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Daniels J, Goebel V
Dominguez-Bernal G,
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Perez-Diaz J, Bayu...
Perez-Diaz J, Bayu...
De Pablos
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Pred. No. 4.4e-
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                                                                                                                                                                                                                                             Rusniok C, Fsihi H, Dehoux
I, Glaser P, Kunst F, Cossar
M, Ng E, Vazquez-Boland JA;
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Best Local Similarity
Matches 115; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM47254 standard;
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                                                                                                                                                                                                                                                                                     Arxula
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                                                                                                                                          Region
                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                             membrane
                                                                                                                                                                                                                                                                                                                                                                                               Yeast; protein production; AXOH; insulin; phytase; hirudin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                        human growth hormone;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FCGLG-GASGGFAEYVVYGEDHMVKLPDSIPDDIGALVEPISVAWH-AVERARFQPGQTA 195
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                                                                                                                                       /note= "ZnADH signature"
188..214
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31.6%;
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Pred. No. 6.3e-26;
1; Mismatches 150;
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                                                                                                                                                                                                                                                                                                                                                                     granulocyte
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 15; Fig 31; 125pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Producing proteins in Arxula yeast, useful e.g. for preparing insulin, by expression under control of specific inducible or constitutive
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N-PSDB; ABA03453, AI
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                                                                                                                                                                                                                                                                                                                     16 ETYPEPEIKNPNDVKIKYSYCGICGTDLKEFTYSGGPVFFPKQGTKDKISGY--ELPLCP
                                                                                      NAVLKAMVPENEGFHAAFDCSGVPQTFTTSIVATGPSGIAVNVAVWGDHPIGFMPMSLTY
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                                                                                                                                                                                PHVRFAACPPTDGTLCKYYTLPEDFCVKLPENVDFEEGALVEPLSVAVHTARLLGIYPGS
                                                                                                                                                                                                 ASLSFCGLGGASGGFAEYVVYGEDHMVKLPDSIPDDIGALVEPISVAWHAVERARFQPGQ
                                                                                                                                                                                                                                                            GHEFSGTVVEVGSGVTSVKPGDRVAVEATSHCSDRSRYKDTVAQDLGLCMACQSGSPNCC 133
                             QEKYATGSMCYTVKDFQEVVKALEDGLISLDKARKMIT 346
                                                                                                                                                                                                                                         GHESSGVVVEVGSEVTSLKVGDRVAMEPGVPDRRSKEYK----
                                                                                                                                                                                                                                                                                                   EERPVPVITDPRDVKIQVKKTGICGSD------VHFWQHG---RIGDYVVEKPMVL 79
                                                          HKILE-LLPNKQAPDVVIDASGAEQSINAGIELLERGGTFGQVAMGRTDYIQFAVSRMAM
                                                                                                                      KVVVFGAGPIGQLCIGVCKAFGASIIGAVDLFEQKLETAKEFGASHTYVPQKGDSHDETA
KEIRFQGVFRYTYGDYELATQLIGDGKIPV--
                                                                                                                                                                                                                                                                                                                                                               107;
                                                                                                                                                                                                                                                                                                                                                                             Similarity
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31.7%;
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                                                                                                                                                                                                                                                                                                                                                              Score 346; DB 23;
Pred. No. 1.1e-25;
0; Mismatches 153;
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KULTURPFLANZENFOR.
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339
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Listing first 45 summaries
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                                                            Query
Match
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Gapop 10.0 , Gapext 0.5
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2013
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1: pir1:*
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G75049 C90939 G85787	S10065 A54674 S64902	AF1918 S16132 F64937	F98227 AB3059 AB0407 F83673	E95295 H64937 S13529
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Qy 241 DPSTCDDAN-AVLKAMVPENEGFHAAFDCSCVPQTFTTSIVATGPSGIAVNVAWGDHPI 299	Db 59 CHKLSNAALFLAMGHEMSGIVSKVGPKVTKVKVGDHVVVDÄASSCADLHCWPHSKFYNSK 118 OY 121 LCMACQSGSPNCCASLSFCGLGGASGGFAEVVVYGEDHMVKLPDSIPDDIGALVEPISVA 180 OY 121 LCMACQSGSPNCCASLSFCGLGGASGGFAEVVVYGEDHMVKLPDSIPDDIGALVEPISVA 180 I	Query Match Query	C;Date: 05-May:1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002. C;Accession: S51962 R;Bussey, H; Kaback, D.B.; Zhong, W.; Vo, D.T.; Clark, M.W.; Fortin, N.; Hall, J.; submitted to the EMBL Data Library, August 1994 A;Description: The sequence of chromosome 1 of Saccharomyces cerevisiae. A;Reference number: S51956 A;Accession: S51962 A;Molecule type: DNA A;Residues: 1-382 <bus> A;Cross-references: EMBL:U12980; NID:g1326053; PID:g595526; GSPDB:GN00001; MIPS:YAL06 A;Genetics: A;Gene: SGD:BDH1; FUN49; MIPS:YAL060W A;Cross-references: SGD:S0000056 A;Map position: 1L C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology F;24-363/Domain: long-chain alcohol dehydrogenase homology</bus>	RESULT 1 \$51962 FUN49 protein - yeast (Saccharomyces cerevisiae) N;Alternate names: protein YAL060w C:Species: Saccharomyces cerevisiae

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L-iditol 2-dehydrogenase BH3949 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C;Accession: E84143 R;Takami, H; Nakasone, K; Takaki, Y; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Nucleic Acids Res. 28, 4317-4331, 2000 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132 A;Accession: E84143 A;Complete type: DNA A;Residues: 1-348 <STO>
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       A;Cross-references: GB:AP001520;
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R;Map position: 1L

C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase; long-chain alcohol dehydrogenase homology <LADH>
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A;Accession: S51961
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ilarity 45.9%;
Conservative 7
     GB:BA000004; NID:g10176401;
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Pred. No. 2.5e-62;
1; Mismatches 130
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August 1994
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-363 <STO>
A;Cross-references: GB:AE004831; GB:AE004091; NID:g9950347; PIDN:AAG07540.1; GSPDB:GN
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                A; Gene: PA4153
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, .; LOTY, S.; Olson, M.V. Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2,3-butanediol dehydrogenase PA4153 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 *sequence_revision 15-Sep-2000 *text_change 31-Dec-2000 C;Accession: C83128
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C; Superfamily:
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                                   PHPLTGLKDQCILGHEFSGEIVRLGNGVTGFAVGQAVAADACQHC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence of Pseudomonas aeruginosa PAO1, 50; MUID:20437337; PMID:10984043
                                                                                                                                                                                                       28.2%; Score 567.5; DB 2; 36.1%; Pred. No. 5.8e-36;
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Pred. No. 3e-36;
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probable alcohol dehydrogenase (EC 1.1.1-) ydjL [similarity] - Bacillus subtilis N;Alternate names: L-iditol 2-dehydrogenase homolog ydjL; sorbitol dehydrogenase homolog C;Species: Bacillus subtilis C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Sep-2000 C;Accession: H69789 C;Accession: H69789 C;Bate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Sep-2000 C;Accession: H69789 C;Bate: Discontain the contained provided the co
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C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homo.
C;Superfamily: alcohol dehydrogenase; zinc
C;Keywords: metalloprotein; NAD; oxidoreductase; zinc
F;22-334/Domain: long-chain alcohol dehydrogenase homology <LADH>
F;171-200/Region: beta-alpha-beta NAD nucleotide-binding fold
F;37,70,152/Binding site: zinc, catalytic (Cys, His, Glu) #status predicted
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A;Residues: 1-346 <KUN>
A;Cross-references: GB:Z99107; GB:AL009126; NID:g2632866; PIDN:CAB12443.1; PID:g2632937
A;Experimental source: strain 168
C;Genetics:
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                                AQDLGLCMACQSGSPNCCASLSFCGLGGASGGFAEYVVYGEDHMVKLPDSIPDDIGALVE 175
                                                                                                                                                     VDKPHPLTNETAPVTMGHEFSGEVVEVGEGVENYKVGDRVVVEPIFATH--
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A;Cross-references: GB:AE005176; PID:g12723828; PIDN:AAK04995.1; GSPDB:GN00f46
A:Experimental source: strain IL1403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKGAEIHPNDIVIKERTVKGIIGY -- RDIFPAVLSLMKEGYFSAD -- - KLVTKKIVLDDL 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DHPIGFMPMSLTYQEKYATGSMCYTVKD-FQEVVKALEDGLISLDKARKMITGKVHLKDG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSAVALYAVRSSKLKAGDKAAVFGCGPIGLLVIEALKAAGATDIYAVELSPERQQKAEEL
LKDGVEKGFKQLIEHKENNVKILVTP
                                                                                                                                                                                                                                                                                                                                                                                                                     MRAAREYDRGDIRIDE-INEPIVK-AGQVGIDVAWCGICGTDLHEFL--DGPIFCPSAEH 70
                                                                                                                                                              VAVWGDHPIGFMPMSLTYQEKYATGSMCYTVKDFQEVVKALEDGLISLDKARKMITGKVH 350
                                                                                                                                                                                                                                                                                                         AEV----FDPSTCDDANAVLKAMVPE--NEGFHAAFDCSGVPQTFTTSIVATGPSGIAVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ETGHYNLSEGSNFIGLGGNGGGLAEKISVDERWVHKIPDNLPLDEAALIEPLS
                                                                                        VAIWG-KPASVDMAKLVIKEANLLGTIAYN-NTHPKTIDLVSTGKIKLD---QFITAKIG
                                                                                                                                                                                                                                       AQVADYFFNPIEDD-----IQAKVHEINEKGVDAAFECTSVQPGFDACLDAIRMGGTVVI
                                                                                                                                                                                                                                                                                                                                                                                  VGYHAVERANLSEKSTVLVVGAGPIGLLTAAVAKAQGH---TVIISEPSGLRRKKAQE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGLCMACQSGSPNCCASLSFCGLGGASGGFAEYVVYGEDHMVKLPDSIPDDIGALVEPIS 178
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J.; E

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LDDLIDKGFDTLIHHNETAVKILVSP

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A; Title: Complete DNA sequence of a serogroup A strain of Neisseria A; Reference number: A81775; MUID:20222556; PMID:10761919
A; Accession: H81925
                                                                                                                                                                                                            probable alcohol dehydrogenase (EC 1.1.1.-) NMA0808 [similarity] -
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-
C:Accession: H81925
         22222
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C;Superfamily:
C;Keywords: oxi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Complete genome sequence of Neisseria meningitidis serogroup B A;Reference number: A81000; MUID:20175755; PMID:10710307 A;Accession: E81178
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Science 287, 1809-1815, Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Arauthors; Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable alcohol dehydrogenase (EC 1.1. C; Species: Neisseria meningitidis C; Date: 31-Mar-2000 #sequence_revision C; Accession: E81178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: serogroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-354 <TET>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                       Species: Neisseria meningitidis;Date: 05-May-2000 #text_change 02-Feb-2001;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
                       Cross-references:
                                          Molecule type: DNA
Residues: 1-354 <PAR>
                                                                           Status: preliminary
                                                                                                                                                  Holroyd, S.; Jagels, K.; ture 404, 502-506, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 KAREŚGYADYILDPSEYDVVAEVKK--LTNGEGYDVAFECTSVNKYLDTLVEACKPAANL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 LVEPISVAWHAVERARFQPGQTALVLGGGPIG--LATILALQGHHAGKIVCSEPALIRRQ
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                                                                                                                                                                                                                                                                                                                                                            IKLDELVSKGFERLIHNNESAVKIIVSPN
                                                                                                                                                                                                                                                                                                                                                                                                                                  VIVSIW-SHPATINVHSVVMKELDVRGTIAY-CNDHAETIKLVEEGKINLE---PFITQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIEPLSVGHHAYVRSGAKEGDVALVGGAGPIGLLLAAVLKAKGI---KVIITELSKARKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHPISGESAPVTMGHEFSGVVYAVGEGVDDIKVGQHVVVEPYIIRDDVPTGEGSNYHLSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DTVAQDLGLCMACQSGSPNCCASLSFCGLGGASGGFAEYVVYGEDHMVKLPDSIPDDIGA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MKAAREYDKGDIRI-EDIPEPTVA-PGTVGINVAWCGICGTDLHEF--MEGPIFIPPCGH
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       source: serogroup
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                                                                                                                                                                   n, M.; James,
K.; Leather,
   serogroup
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54;
 GB:AL157959; NID:g7379424; PIDN:CAB84091.1; A, strain Z2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MNFIGLGGCGGGLSEKIAVKRRWVHPISDKIPLDQAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GB:AE002098; NID:g7225832; B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 537;
Pred. No. 1.
                                                                                                                                                                   S.; MC
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                                                                                                                                                                                                                                                                                                                                                            353
                                                                                                                                                               .; Bentley, S.D.; Churcher, C.; Klee, Moule, S.; Mungall, K.; Quail, M.A.;
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.2e-33;
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                                                                                                                                                                                                                                                              Neisseria
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                                                                                                                             menigitidis Z2491.
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strain MC58
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                     PID:g73795
                                                                                                                                                                 S.R.; More Rajandream
                                                                                                                                                                                                                                                            meningitid
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LCMACQSGSPNCCASLSFCGLGGASGGFAEYVVYGEDHMVKLPDSIPDDIGALVEPISVA 180

56 61

AHPLSGCRAPLTLGHEFCGVVAALGPGVEGPRIGDRVAVEPEYRC

KDKISGYELPLCPGHEFSGTVVEVGSGVTSVKPGDRVAVEATSHCSDRSRYKDTVAQDLG

120

101

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A; Gene:
C; Superf
                                                                                                                                                                                                                                                                                                                                                                                                                                             probable alcohol dehydrogenase (2n-dependent) PA4097 [imported] - Pseudomon
C; Species: Pseudomonas aeruginosa
C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
B83133
                                                                                                                                                                                                         A;Cross-references: GB:AE004826; GB:AE004091; NID:g9950296; PIDN:AAG07484.1; GSPDB:GNA;Experimental source: strain PAO1
                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-352 <STO>
                                                                                                                                                                                                                                                                                                                     A; Title: Complete genome sequence of Pseudomonas aeruginosa A; Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                        A; Accession: B83133
                                                                                                                                                                                                                                                                                                                                                                                               adman, S.;
                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                            Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                              R;Stover, C.K.; Pham, X.Q.;
                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession:
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A;Gene: NMAO808
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase
C;Keywords: oxidoreductase
                                                                           Matches
                                                                                                                                                     Superfamily:
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Best Local
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                                                                                            Local
                   PA4097
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MKALRWHAARDLRLSEL--ERQAPRPGEVELEVAYCGICGSDLHE--YQSGPHSIP-QAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FAKELGAE--VFDPSTCDDANAVLKAMVPENEGFHAAFDCSGVPQTFTTSIVATGPSGIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIVSIW-SHPATVNVHSVVMKELDVRGTIAY-CNDHAETIKLVEEGKINLE---PFITQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KARESGVADYILDPSEVDVVEEVKK--LTNGEGVDVAFECTSVNKVLDTLVEACKPAANL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIEPLSVGHHAYVRSGAKAGDVALVGGAGPIGLLLAAVLKAKGI---KVIITELSKARKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DTVAQDLGLCMACQSGSPNCCASLSFCGLGGASGGFAEYVVYGEDHMVKLPDSIPDDIGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHPISGESAPVTMGHEFSGVVYAVGEGVDDIKVGQHVVVEPYIIHDDVPTGEGSNYHLSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDKISGYELPLCPGHEFSGTVVEVGSGVTSVKPGDRVAVE-----ATSHCSDRSRYK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKAARFYDKGDIRI-EDIPEPTVA-PGTVGINVAWCGICGTDLHEF--MEGPIFIPPCGH
                                                                                                                                                                                                                                                                                                                                                                                                 Yuan,
                                                                                                                                                                                                                                                                                                                                                                      Tuan, Y.; Bro
                                                                                           Similarity
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                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             Brody,
                                                                                                                                                 dehydrogenase; long-chain alcohol dehydrogenase
                                                                                           22.6%;
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                                                                                                                                                                                                                                                                                                                                                                                           Erwin, A.L.; Mizoguchi, S.D.;
L.L.; Coulter, S.N.; Folger, 
                                                                           55;
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                                                                                           Score 455.5;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 534; DB 2;
Pred. No. 2.1e-33;
                                                                           Mismatches
                                                                                         5; DB 2;
?.2e-27;
                                                                           162;
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                                                                         Indels
                                                                                                            Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                           P.; Hickey, A.; Larbig,
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                     opportunistic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C:Genetics:
A:Gene: Atu4740
A:Map position: linear chromosome
C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE008689; PIDN:AAL45534.1; PID:917743246; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      zinc-binding dehydrogenase Atu4740 [imported] - Agrobacterium tumefaciens (strain c; Species: Agrobacterium tumefaciens (c; Sciate; L-Jan-2002 #text_change 01-Feb-2002 R; Wood, D.W.; Setubal, J.C.; Koul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; M.; Karp, P.; Romero, P.; Zhang, S.; Science 294, 2317-2323, 2001 A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Beter, E.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-357 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58
A;Reference number: AB2577; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 21.0%; Score 422.5; DB 2
Best Local Similarity 28.5%; Pred. No. 7.6e-25;
Matches 109; Conservative 75; Mismatches 160
                                                                        293 VW-GDHPIGFMPMSLTYQEKYATGSMCYTVKDFQEVVKALEDGLISLDKARKMITGKVHL
                                                                                                                                                                                                                                                                                                                                            115
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                                  LHPHENPIDW---FQVTFRDLEIKGSWAYPTHYWPRVIRLIASGLL---PATKIVTKRITL
                                                                                                                                                    LGAEV--FDPSTCDDANAVLKAMVPENEGFHAAFDCSGVPQTFTTSIVATGPSGIAVNVA
                                                                                                               VIRDVITINEKR-DNVGDVVRSATEGKVGCDVAIECVGNEHALKACVDAVRKQGVVVQTG
                                                                                                                                                                                                                                                                              EPSAVAVYACDRGGYTAGNSVLVTGAGPIGMLTLLAARAAGATQLFVSDLNDARLELARN
                                                                                                                                                                                                                        EPISVAWHAVERARFQPGQTALVLGGGPIGLATILALQGHHAGKIVCSEPALIRRQFAKE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKGLLYYGTNDIRYSETVPEPEIKNPNDVKIKVSYCGICGTDLKEFTYSGGPVFFPKQGT
                                                                                                                                                                                                                                                                                                                                                               PHPFTGAHGPQILGHEFGGVYEAIGDGVTSVNVGDRVSIQPLIMPRSGDYFADRGLF---
                                                                                                                                                                                                                                                                                                                                                                                              KDKISGYELPLCPGHEFSGTVVEVGSGYTSVKPGDRVAVE-----ATSHCSDRSRYKDT
                                                                                                                                                                                                                                                                                                                                                                                                                                              MRALRFHAAKDLRI-EDIAEPKRPGPGQVLVRNRFVGICGTDLHEYSY--GPIFIPTE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEALLRDK-SQLKVLVNPN 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RLDAFDLVNRELRLLGSVGY--RDAYPELTALLADGRLDLARA---VTRSVPLEQAVEHG
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L-iditol 2-dehydrogenase (EC 1.1.1.14) - Bacillus subtills N;Alternate names: glucitol dehydrogenase; polyol dehydrog C;Species: Bacillus subtilis C;Species: Bacillus subtilis C;Cate: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_c C;Accession: A45052; E69638; I39862 C;Accession: A45052; E69638; I39862 C;Accession: A45052; Kong, S.L. J. Biol. Chem. 267, 24989-24994, 1992 A;Title: Sorbitol dehydrogenase from Bacillus subtilis. Pu. A;Reference number: A45052; MUID:93094198; PMID:1460002 A;Accession: A45052 DNA
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldner, Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A;Reference number: A97359; PMID:11743194
A;Accession: D98148
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: AGR_L_281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C:Species: Agrobacterium tumefaciens
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C:Accession: D98148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE007870; PIDN:AAK88710.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; MOIECUIE type: DNA
A; Residues: 1-397 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule
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                                                               371 DTAVTEGFDALLDPAGTHLKILI
                                                                                                 352 KDGVEKGFKQLIEHKENNVKILV
                                                                                                                                               316
                                                                                                                                                     293 VW-GDHPIGFMPMSLTYQEKYATGSMCYTYKDFQEVVKALEDGLISLDKARKMITGKVHL : |:: | | :: | |:: | |:: | |:: |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 352 KDGVEKGFKQLIEHKENNVKILV
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                                                                                                                               LHPHENPIDW---FOVTFRDLEIKGSWAYPTHYWPRVIRLIASGLL---PATKIVTKRITL
                                                                                                                                                                                                     VIRDVITINPKR-DNVGDVVRSATEGKVGCDVAIECVGNEHALKACVDAVRKQGVVVQTG
                                                                                                                                                                                                                                         LGAEV--FDPSTCDDANAVLKAMVPENEGFHAAFDCSGVPQTFTTSIVATGPSGIAVNVA 292
                                                                                                                                                                                                                                                                               EPSAVAVYACDRGGVTAGNSVLVTGAGPIGMLTLLAARAAGATQLFVSDLNDARLELARN
                                                                                                                                                                                                                                                                                                       EPISVAWHAVERARFOPGOTALVLGGGPIGLATILALOGHHAGKIVCSEPALIRRQFAKE 234
                                                                                                                                                                                                                                                                                                                                                       ------HLSTQLALVGLSWDGGGMAEAALVNEYNVQKIPDEMTDEEAALV
                                                                                                                                                                                                                                                                                                                                                                                                                             PHPFTGAHGPQILGHEFGGVVEAIGDGVTSVNVGDRVSIQPLIMPRSGDYFADRGLF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KDKISGYELPLCPGHEFSGTVVEVGSGVTSVKPGDRVAVE-----ATSHCSDRSRYKDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MRALRFHAAKDLRI-EDIAEPKRPGPGQVLVRNRFVGICGTDLHEVSY--GPIFIPTE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dehydrogenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.0%; Score 422.5; DB 2; 28.5%; Pred. No. 8.7e-25; tive 75; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      long-chain alcohol dehydrogenase homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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10-Mar-1994 #text_change

03-Nov-2000

sorbitol dehydrogen

Purification,

characterizati

subtilis dehydrogenase;

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A; Title: Transcriptional regulation of the Bac A; Reference number: 139862; MUID:94253000; PMII A; Accession: 139862
A; Status: preliminary; translated from GB/EMBI. A; Molecule type: DNA A; Molecule type: DNA A; Cross-reference.
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A; Residues: 1-35 <NCl>
A; Cross references: GB:M96947; NID:g304152; PIDN:AAA22508.1; PID:g304153
A; Cross references: GB:M96947; NID:g304152; PIDN:AAA22508.1; PID:g304153
A; Cross references: GB:M96947; NID:g304152; PIDN:AAA22508.1; PID:g304153
A; Note: sequence extracted from NCBI backbone (NCBIN:120108, NCBIP:120111)
A; Note: sequence extracted from NCBI backbone (NCBIN:120108, NCBIP:120111)
A; Note: sequence extracted from NCBI backbone (NCBIN:120108, NCBIP:120111)
A; Note: sequence extracted that the third ligand of the catalytic zinc is 156-clu
A; Note: presents arguments that the third ligand of the catalytic zinc is 156-clu
A; Note: presents arguments that the third ligand of the catalytic zinc is 156-clu
A; Note: presents arguments that the third ligand of the catalytic zinc is 156-clu
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A; Note: presents arguments that the third ligand is 1
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A; Residues: 1-353 <KUN>
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A; Experimental source: strain v
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIINIREQDALEEIKT-ITNDRGVDVAWETAGNPAALQSALASVRRGGKLAIVGLPSQNE
                                                                                                                                                                                                                                                                                                   VAWHAVERARFQPGQTALVLGGGPIGLATILALQGHHAGKTVCSEPALIRRQFAKELGAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGLCMACQSGSPNCCASLSFCGLGGASGGFAEYYVYGEDHMVKLPDSIPDDIGALVEPIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGRIGNYVVEKPFILGHECAGEIAAVGSSVDQFKVGDRVAVEPGVTC----
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                                                                                                   VFDPSTCDDANAVLKAMVPENEGFHAAFDCSGVPQTFTTSIVATGPSG-
                                                                                                                                                                                                      -GRCEACKEGRYNLCPDVQFLATPPVDGAFVQYIKMRQDFVFLIPDSLSYEEAALIEPFS
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249-256, 1997
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Pred. No. 8.9e-24;
6; Mismatches 155
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PMID:8195086
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hypothetical protein R04B5.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C;Accession: T23889
R;Wilkinson, J.
Submitted to the EMBL Data Library, April 1996
A;Reference number: Z19814
A;Accession: T23889
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A;Experimental source: clone R04B5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-347 <WIL>
A; Cross-references: EMB
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A; Introns: 62/3; 138/2:
C; Superfamily: alcohol
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                ---PMIVGHETSGIVSEVGNEVKHLKVGDRIAMEPGLPCK--
                                                                                                                                                                                                                                                                                                                                                            YELPLOPGHEFSGTVVEVGSGVTSVKPGDRVAVEATSHCSDRSRYKDTVAQDLGLCMACQ 126
                                                                                                                                                                                                                                                                                                                                                                                                YGVDDLRL-EQVPIPK-PGPNQVLVKVHTVGICGSDVHYWTHGAIGPFVVKE------
                                                                                                                                                                                                                                                                                                                                                                                                                              YGTNDIRYSETVPEPEIKNPNDVKIKVSYCGICGTDLKEFTYSGGPVFFPKQGTKDKISG
                                                                                                                              VKGKSLDAVKSEIITALGDQQPDVCIECTGAQPSIETAITTTKSGGVIVLVGLGADRVEI
                                                                                                                                                                                                                              ARFOPGQTALVLGGGPIGLATILALOGHHAGKIVCSEPALIRROFAKELGAEVFDPSTCD
                                                                                                                                                                                                                                                                TGRYNLCPEMRFFATPPVHGTLSRFVVHDADFCFKLPDNLSFEDGALIEPLSVAIHACRR
                                                                                                                                                                                                                                                                                   SGSPNCCASLSFCGLGGASGGFAEYVVYGEDHMVKLEDSIPDDIGALVEPISVAWHAVER 186
                                                                                                                                                              DANAVLKAMVPE-----NEGFHAAFDCSGVPQTFTTSIVATGPSGIAVNVAVWGDH---
                                                                                                                                                                                                GNVQMGHRVLVLGAGPIGVLNLITAKAVGAGKVVITDLDDGRLALAKKLGAD----ATIN
EAFKR--TOKADVIKVFI 345
                                                                PI----IESATREVDMRGIFRY-VNCYPTAIELISSGKLNLSGLT-----RAHYKLEETQ
                                                                                            PIGFMPMSLTYQEKYATGSMCYTVKDFQEVVKALEDGLISLDKARKMITGKVHLK-DGVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62/3; 138/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; 221/2; 259/3; 300/2
dehydrogenase; long-chain alcohol dehydrogenase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.2%; Score 386.5; DB 2; 29.6%; Pred. No. 4.3e-22; tive 62; Mismatches 151;
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L-iditol 2-dehydrogenase (EC 1.1.1.14) - silkworm N; Alternate names: sorbitol dehydrogenase C; Species: Bombyx mori (silkworm) C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 C; Accession: S32484 R; Nilmi, T.; Yamashita, O.; Yaginuma, T.

#text_change 16-Jun-2000

Eur. J. Biochem. 213, 1125-1131, 1993 A;Title: A cold-inducible Bombyx gene

O.; Yaginuma, 125-1131, 1993

encoding a protein similar to

mammalian

sorbito

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C;Function:

A;Description: catalyzes the oxidation by NAD+ of sorbitol to fructose
A;Description: catalyzes the oxidation by NAD+ of sorbitol to fructose
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C;Keywords: homotetramer; metalloprotein; NAD; oxidoreductase; zinc
F;25-337/Domain: long-chain alcohol dehydrogenase homology <LADH>
F;170-199/Region: beta-alpha-beta NAD nucleotide-binding fold
F;40,65,151/Binding site: zinc, catalytic (Cys, His, Gin) #status predicted
F;95,98,101,109/Binding site: zinc, noncatalytic (Cys) #status predicted
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A;Residues: 1-348 <NII>
A;Cross-references: EMBL:D13371; NID:g217259; PIDN:BAA02634.1; PID:g217260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: B72381
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A;TILLe: Evidence for lateral gene transfer between Archaea and Bacteria from genome A:Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: B72381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hugarrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
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                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-395 <ARN>
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                                                                                                                                                                                                                                              A; Experimental source: strain MSB8
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LLYYGTNDIRYSET----VPEPEIKNPNDVKIKVSYCGICGTDL-KEFTYSGGPVFFPKQ 58
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                                                                                                 18.4%; Score 370; DB 2; 34.0%; Pred. No. 9.2e-21;
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                                FTTSI--VATGPSGIAVNVAV 293
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                                                                     ASKVILSEPSEVRRNLAKELGADHVIDPTKENFVEAVLD--YTNGLGAKLFLEATGVPQL
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                                                                                                                                                                      HMVKLPDSIPDDIGALVEPISVAWHA - - VERARFQPGQTALVLGGGPIGLATILALQGHH 215
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PRIOR FILING DATE: 1997-08-14
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APPLICANT: LYNN DOUCETTE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: EPIDERWIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
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US-09-347-803-27
                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08466548B Patent No. 6022712
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 27
LENGTH: 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 27, Application US/09347803 Patent No. 6274379
                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER FILING DATE: July 15, 1998
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kinney, Tony
APPLICANT: Orozco, Buddy
TITLE OF INVENTION: Plant Sorbitol Biosynthetic Enzymes
FILE REFERENCE: BB-1176
CURRENT APPLICATION NUMBER: US/09/347,803
CURRENT FILING DATE: 1999-07-02
CURRENT FILING DATE: 1999-07-02
CURRENT APPLICATION NUMBER: 60/092,952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 371
TYPE: PRT
ORGANISM: Malus domestica
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                             APPLICANT: sarthy, aparna v
APPLICANT: schopp, cynthia w
TITLE OF INVENTION: ENHANCED YEAST EXPRESSION USING
TITLE OF INVENTION: DEHYDROGENASE GENE
TITLE OF INVENTION: DEHYDROGENASE GENE
                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                              263 HAAFDCSGVPQTFTTSIVATGPSG
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                                              ZIP:
                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGVTSVKPGDRVAVEATSHCSDRSRYKDTVAQDLGLCMACQSGSPNCCASLSFCGLGGAS 145
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                                            60064-3500
                                                                                              SEE: ABBOTT LAORTORIES
: ONE ABBOTT PARK ROAD
ABBOTT PARK
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                                                                             ILLINOIS
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                                                                                                                                                                                                          FROM YEAST SORBITOL
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US-07-998-226F-2
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                                                                                                                                                                                                                                                         Sequence 2, Application US/07998226F Patent No. 6033898
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Best Local Similarity
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                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                      NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LAORTORIES
                                                                                                                                            TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                    APPLICANT: sarthy, aparna v
APPLICANT: schopp, cynthia w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                         348 VVKTII 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 TALVLGGGPIGLATILALQGHHAGKIVCSEPALIRRQFAKELGA-EVFDPS--TCDDANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 PHMAFAATPPIDGTLVKYYLSPEDFLVKLPEGVSYEEGACVEPLSVGVHSNKLAGVRFGT 172
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               COUNTRY:
                                    STATE:
                                                                       STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/998,226 FILING DATE: 30-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: WALSH, ANDREA C
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QEKYATGSMCYTVKDFQEVVKALEDGLISLDKARKMITGKVHLKDGVEKGFKQLIEHKEN 368
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60064-3500
                                                   ABBOTT PARK ROAD
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GY: linear
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                                                                                                                                                                              ENHANCED YEAST EXPRESSION USING
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Pred. No. 2.1e-29;
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NAME: WALSH, ANDREA C
REGISTRATION NUMBER: 34988
REFERENCE/DOCKET NUMBER: 528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                              Sequence 2, Application PC/TUS9312560 GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US
APPLICATION NUMBER: US
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                          APPLICANT: sarthy, aparna v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                   348 VVKTII 353
                                                                                                                                                                                                                                                                                                                                                                                                     369 NVKILV 374
                                                                                                                                                                                                                                                                                                                                                                                                                                292 KEMKLIGCFRYSFGDYRDAVNLVATGKVNV---KPLITHKFKFEDAA-KAYDYNIAHGGE 347
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                                      COUNTRY: US
ZIP: 60064-3500
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                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                       T: ONE ABBOTT PARK ROAD ABBOTT PARK
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                                                                                                                         ABBOTT LAORTORIES
Floppy disk
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FROM YEAST SORBITOL
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RESULT 6
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                                                                                                                                                                                                                                          Sequence 20, Application US/09347803 Patent No. 6274379 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity Matches 111; Conserv
                        APPLICANT: Kinney, Tony
APPLICANT: OTOZCO, Buddy
TITLE OF INVENTION: Plant Sorbitol Biosynthetic |
FILE REFERENCE: BB-1176
CURRENT APPLICATION NUMBER: US/09/347,803
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,952
EARLIER FILING DATE: July 15, 1998
NUMBER OF SEQ ID NOS: 27
SOFTWARF: MICROSOFT OFFICE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
              SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                        APPLICANT: Famodu, La
APPLICANT: Hitz, Bill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 0: FILING DATE: 30-DEC-1992 ATTORNEY/AGENT INFORMATION:
ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309 QEKYATGSMCYTYKDFQEVVKALEDGLISLDKARKMITGKVHLKDGVEKGFKQLIEHKEN 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 PHMAFAATPPIDGTLVKYYLSPEDFLVKLPEGVSYEEGACVEPLSVGVHSNKLAGVREGT 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 GHEFSGTVVEVGSGVTSVKPGDRVAVEATSHCSDRSRYKDTVAQDLGLCMACQSGSPNCC 133
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REFERENCE/DOCKET NUMBER: 5
REFERENCE/DOCKET NUMBER: 5
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REGISTRATION NUMBER: 34988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GHESSGQVVEVGDAVTRVKVGDRVAIEP----GVPSRYSDET------KEGRYNLC 112
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30.3%;
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Pred. No. 2.1e-29;
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; TYPE: PRT ; ORGANISM: Glycine US-09-347-803-20

LENGTH: 316 TYPE: PRT

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US-09-347-803-22
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LENGTH: 301
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Patent No. 62743
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Best Local Similarity
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Best Local Similarity
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CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER FILING DATE: July 15, 1998
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kinney, Tony
APPLICANT: Orozco, Buddy
TITLE OF INVENTION: Plant Sorbitol Biosynthetic Enzymes
FILE REFERENCE: BB-1176
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                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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                                    203 IGLATILALQGHHAGKIVCSEPALIRRQFAKELGAEV---FDPSTCDDANAVLKAMVPEN 259
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                                                                                                                                                      71
                                                                                                                                                                                                                                  25 PYDVRVRMKAVGICGSDVHYLKEMRIAH---FVVKE-----PMVIGHECAGIIE 70
                                                                                                                                                                                                                                                                        26 PNDVKIKVSYCGICGTD---LKEFTYSGGPVFFPKQGTKDKISGYELPLCPGHEFSGTVV 82
                                                                                                              GASGGFAEYVVYGEDHMVKLPDSIPDDIGALVEPISVAWHAVERARFQPGQTALVLGGGP 202
                                                                                                                                                        EVGDGVKHLAVGDRVALEPGISC------WRCRHCKGGRYNLCDDMKFFATP 116
                                                                                                                                                                                            EVGSGVTSVKPGDRVAVEATSHCSDRSRYKDTVAQDLGLCMACQSGSPNCCASLSFCGLG 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATILALQGHHAGKIVCSEPALIRRQFAKELGA-EVFDPST--CDDANAVLKAMVPENEGF 262
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                                                                              PYHGSLADQIVHPGDLCFKLPDNVSLEEGAMCEPLSVGVHACRRADVGAEKSVLIMGAGP 176
IGLVTMLSARAFGAPRIVIADVDDHRLSVAKSLGADAVVKVSGNTEDLAGEIERIQAAMG
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Pred. No. 2.8e-28;
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US-09-347-803-16
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; ORGANISM: Zea
US-09-347-803-16
                                                                                                                                                                                                                                                                                                          US-09-134-001C-4483
                                                                                                                                                                         Sequence 4483, Application US/09134001C
Sequence 1483, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: LYNN DOUCET ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                        FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/347,803
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kinney, Tony
APPLICANT: Orozco, Buddy
TITLE OF INVENTION: Plant Sorbitol Biosynthetic
FILE REFERENCE: BB-1176
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PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER: OF SEQ ID NOS: 5674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYDVRVRMKAVGICGSDVHYLREMRIAH --- FVVKE------PMVIGHECAGVVE 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDIDVSLDCAGFSKTMSTALEATRPGGKVCLVGMGHNE----MTLPLAAREVDVVGVFRY 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGFHAAFDCSGVPQTFTTSIVATGPSGIAVNVAVWGDHPIGFMPMSLTYQEKYATGSMCY 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103;
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Pred. No. 8.4e-26;
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEG ID NOS: 5674
SEG ID NO 3003
LENGTH: 381
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
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; LENGTH: 382
; TYPE: PRT
; ORCANISM: Staphylococcus epidermidis
US-09-134-001C-4483
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US-09-134-001C-3003
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                                                                                                                                                                                                                             Query Match
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197 VKPGCTVAIVGAGPVGLAALLTAQFYSPSKIIMIDLDDNRLETAKELGATHLINSKETET 256
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                                                                                                                14 YSETVPEP----EIKNP--NDVKIKVSYCGICGTDLKEFTYSGGPVFFPKQGTKDKISGY 67
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68
                                           89
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                                                                                                                                                                               Local Similarity 24.4 es 96; Conservative
                             ELPLCPGHEFSGTVVEVGSGVTSVKPGDRVAVEATSHCSDRSRYKDTVAQDLGLCMACQS 127
                                                                                          YKESKPLKIEYLELDNPSEHEVLIKIHAAGLCHSDLSVI---
PLPMALGHEASGEVIKVGKAVTRVSEGDHVVCTFIPSC---
                                                                                                                                                                               13.2%; Score 265.5; DB 4; 24.4%; Pred. No. 2.3e-19; tive 54; Mismatches 152;
                                                                                                                                                                                                                             Length 381;
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                                                                                                                                                                                    Indels 91;
                                                                                          ---NGNRPR---- 67
-- GKCIPCKE 113
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APPLICANT: KOJIMA, TOMOKO APPLICANT: KANAMOTO, HIROAKI APPLICANT: KANAMOTO, HIROAKI APPLICANT: KANAMO, NACKI ITTLE OF INVENTION: MOVEL ENZYME, A METHOD TO PREPARE SAID TITLE OF INVENTION: MOVEL ENZYME, A METHOD TO PREPARE SAID TITLE OF INVENTION: MOVEL ENZYME, A METHOD TO PREPARE SAID TITLE OF INVENTION: MOVEL ENZYME, A DANA SEGMENT ENCODING SAID ENZYME, A TRANSFORMANT TITLE OF INVENTION: CONTAINING SAID DNA SEGMENT AND A METHOD OF PREPARING TITLE OF INVENTION: CONTAINING SAID DNA SEGMENT AND A METHOD OF PREPARING TITLE OF INVENTION: CONTAINING SAID DNA SEGMENT AND A METHOD OF PREPARING TITLE OF INVENTION: CONTAINING SAID DNA SEGMENT AND A METHOD OF PREPARING TITLE OF INVENTION: CONTAINING SAID DNA SEGMENT AND A METHOD OF PREPARING TITLE OF INVENTION: CONTAINING SAID ENZYME RUBBER OF SEQUENCES: 11 CORRESSEE: OBLOW, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: OBLOW, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, APPLICATION NUMBER: US SOMEWAY. APPL	11 114 GREALCENGALISNEKGEMLEGGMRLSNDEGKVYHHLGISGFAEYSVVSENSIVKIDKKIP 114 GREALCENGAISNEKGEMLEGGMRLSNDEGKVYHHLGISGFAEYSVVSENSIVKIDKKIP 168 DD	128 GSBNCCASI.SECGI.GGASGGFAEYVVYGEDHMVKLPDSIP 167

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tent No.
                                  FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC competible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NOVEL ENZYME, A METHOD TO PREPARE SAID TITLE OF INVENTION: ENZYME, A DNA SEGMENT ENCODING SAID ENZYME, TITLE OF INVENTION: CONTAINING SAID DNA SEGMENT AND A METHOD OF
                                                                                             CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 QQYLLVTRPRNLSRIPDNVSADVAAASTDAVLTPYHAIKMAQVSPTSNILLIGAGGLGGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292 LDDVLKLVSEGKV-----KPVVRSAKLKE-----LPEYIEKLRNNAYEGRVVFNP 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 AAFDCSGVPQTFTTSIVATGPSGIAVNVAVWGDHPIGFMPMSLTYQEKYATGSMCYTVKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 AIQVAKAFGA-KVTVLDKKKEARDQAKKLGAD-----AVYETL-PESISPGSFS
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                                                                                                                                                                                                                                                                                                             STATE: Virginia COUNTRY: U.S.A.
APPLICATION NUMBER: JP 5 FILING DATE: 28-DEC-1993
                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                      FILING DATE:
                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 IKVSYCGICGTDLKEFTYSGGPVFFPKQGTKDKISGYELPLCPGHEFSGTVVEVGSGVTS
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les 92; Conserv
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amino acid
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25.8%;
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Pred. No. 3e-17;
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20 EPEIKNP----NDVKIKVSYCGICGTD--LKEFTYSGGPVFFPKQGTKD-KISGYELPLC 72

Matches

Conservative

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Gaps

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US-09-504-358-18
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                                                                                                                                          NUMBER OF SEQ ID NOS: 49
SOFTWARE: Microsoft Office 97
SEQ ID NO 18
LENGTH: 352
                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18, Appl
Patent No. 636537
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                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: 60/120,702
EARLIER FILING DATE: 1999-February-19
NUMBER OF SEQ ID NOS: 49
                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/504,358
CURRENT FILING DATE: 2000-02-15
                                                                                                                                                                                                                                                                                                   APPLICANT: ROUVIERE, Pierre E.
APPLICANT: BIZOSTOWICZ, PATIICIA C.
TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIA
FILE REFERENCE: BC1001 US NA
                                                                                                                          TYPE: PRT
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FQEVVKALEDGLISLDKARKMITGKVHLKDGVEKGFKQLIEHKENNV---KILVTP 376
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Score 236; DB 4; Length 352;
Pred. No. 2.6e-16;
0; Mismatches 154; · Indels
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SOFTWARE: MICROSOFT OFFICE 97
SEQ ID NO 18
LENGTH: 352
TYPE: PRT
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Patent No. 6465224
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rouviere, Pierre E. APPLICANT: Brzostowicz, Patricia C.
       223
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                                                                                                                                                                                                                              70
                                                                                                                                                                                                                                                                   73
                                                                                                                                                                                                                                                                                                      15
                                                                                                                                                                                                                                                                                                                                                                          Match 11.7%; Score 236; DB 4; Local Similarity 28.1%; Pred. No. 2.6e-16; les 104; Conservative 40; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                         20
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TL----TVNSKNATSHDLVEAAGGQFIAIIDLVNTGDTVALAFDALSRAGKIVQVGLFGG
                                                                                                                                                                                  CASLSFCGLGGASGGFAEYVVYGEDHMVKLPDSIPDDIGAL-VEPISVAWHAV-----
                                      EVFDPSTCDDANAVLKAMVPENEG-FHAAFDCSGVPQTFTTSIVATGPSGIAVNVAVWGD
                                                                                                                                                                                                                            MGHETVGEVVEVGEDVTDVAVGDTCLAFPWIGC --
                                                                           SYSSARKATATVNPDEPIGVMGVGGVGMMTVAALVALGHKNIIAIDVSDENLASAQELGA
                                                                                                                                                   CDNGRALGI-IQFGGFAEYLL------LPDQRYAIDVAGVDPAWAATLACSGVT 162
                                                                                                                                                                                                                                                                                                    EIELDRPKPMGREVLLKVTHAGVCHTDTHVQDGGYDLG----SRGTLDMSTRGVTYPCV
                                                                                                                                                                                                                                                                                                                                     EPEIKNP----NDVKIKVSYCGICGTD--LKEFTYSGGPVFFPKQGTKD-KISGYELPLC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNGRALGI-IQFGGFAEYLL-------LPDQRYAIDVAGVDPAWAATLACSGVT 162
                                                                                                                                                                                                                                                               PGHEFSGTVVEVGSGVTSVKPGDRVAVEATSHCSDRSRYKDTVAQDLGLCMACQSGSPNC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGVEKGFKQL 362
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                                                                                                              ---ERARFQPGQTALVLGGGPIGLATILALQGHHAGKIVCSEPALIRRQFAKELGA 237
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                                                                                                                                                                                                                                                                                                                                                                                                            Length 352;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/347,878C
CURRENT FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 52
LENGTH: 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Yuan, Chong
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
FILE REFERENCE: 25885-1651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 52, Application Patent No. 6376210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 37
                                                                                                                                                                                                   174 CGFSTGYGAAVKTGKVKPGSTCVVFGLGGVGLSVIMGCKSAGASRIIGID--LNKDKFEK
333 TEFLAKKFDLD----QLITH
                               346 TGKVHLKDGVEKGFKQLIEH 365
                                                                   290 VVVGV---
                                                                                               289 VNVAVWGDHPIGFMPMS---LTYQEKYATGSMCYTVKDFQEVVKALEDGLISLDKARKMI 345
                                                                                                                                 232 AMAVGATECISPKDSTKPISEVLSEMTGNNVGY--TFEVIGHLETMIDALASCHMNYGTS
                                                                                                                                                                                                                                                                      114 RSDITGRGVLADGTTRFTCKGKPVHHFMNTSTFTEYTVVDESSVAKIDDAAPPEKVCLIG
                                                                                                                                                                                                                                                                                                        135 SLSFCGLGGASGG-----
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                                                                                                                                                                                                                                                                                                                                                                                                        23 SIEEIEVAPPKTKEVRIKILATGICRTD--DHVIKGTMV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                        17 TVPEPEIKNP--NDVKIKVSYCGICGTDLKEFTYSGGPVFFPKQGTKDKISGYELPLCPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 25.3 es 96; Conservative
                                                                                                                                                                 EL---GAEVFDP-STCDDANAVLKAMVPENEGFHAAFDCSGVPQTFTTSIVATGPS-GIA
                                                                                                                                                                                                                                    -PISVAW-HAVERARFQPGQTALVLGGGPIGLATILALQGHHAGKIVCSEPALIRRQFAK
                                                                                                                                                                                                                                                                                                                                      HEATGIVESIGEGVTTVKPGDKVIPLFLPQCRE------CNACRNPDGNLCI 113
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                                                                 PPSAKMLTYDP----MLLFTGRTWKGCVFG--
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 348
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Pred. No. 5.2e-16;
57; Mismatches 142;
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                                                                                                                                                                                                                                                                                                      ----FAEYVVYGEDHMVKLPDSIPDDIGALVE
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Search completed: May 2, 2003, 13:05:55 Job time: 240 secs

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PRIOR FILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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SEQ ID NO 11975
LENGTH: 352
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Best Local Similarity 33.5%;
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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    329
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FILING DATE: 2000-11-27
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                                                                                                                                                              LDARDGDTA----ARLREGGALDCAFEAAGSQASLDAALASLRKGGELVLVSLMGE--V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MKALRWHAARDLRLSEL--ERQAPRPGEVELEVAYCGICGSDLHE--YQSGPHSIP-QAE 55
FEALLRDK-SQLKVLVNPN 346
                                         FKQLIEHKENNVKILVTPN 377
                                                                                  RLDAFDLVNRELRLLGSVGY - - RDAYPELIALLADGRLDLARA - - - VTRSVPLEQAVEHG
                                                                                                                       GEMPMSLTYQEKYATGSMCYTVKD-FQEVVKALEDGLISLDKARKMITGKVHLKDGVEKG
                                                                                                                                                                                                       FDPSTCDDANAVLKAMVPENEGFHAAFDCSGVPQTFTTSIVATGPSGIAVNVAVWGDHPI
                                                                                                                                                                                                                                                                                                                                ECRYCREGRYNLCESMGFIGLMG-DGGFAERARVPAYMLHRLPDAVGFRQAAVLEPAAVA 160
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SOFTWARE: PatentIn Ver.
SEQ ID NO 53
LENGTH: 350
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PRIOR FILING DATE: 1995-01-03
PRIOR APPLICATION NUMBER: US 08/110,672
PRIOR FILING DATE: 1993-08-24
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PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 08/790,585
PRIOR FILING DATE: 1997-01-29
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CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: PCT/FI01/00051
PRIOR FILING DATE: 2001-01-22
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APPLICANT: Ojamo Heikki
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                                     341 ARKMITGKVHLKDG---VEKGFKQ 361
                                                                                                                                                           207
                                                                                                                                                                                                                                                                                                                                         117 QDLGLCMACQSGSPNCCASLSFCGLGGASGGFAEYVVYGEDHMVKLPDSIPDDIGALVEP
                                                                                                                 291 VAVWGDHPIGFMPMSLTYQEKYATGSMCYTVK-----DFQEVVKALEDGLISLDK----
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                                                                             AGV----PYGDVALTREQFEKIVRSEL--TVKGTWFGNSFPFPGKEWSAGLYHMQKGDMN
                                                                                                                                                           ADI----C--INAKEKNIVEEIKRLTDGDGADIVIESAGTPLTCGQVLLLAKKGGTVLY
                                                                                                                                                                                                   AEVFDPSTCDDANAVLKAMVPE-----NEGFHAAFDCSGVPQTFTTSIVATGPSGIAVN
                                                                                                                                                                                                                                      VCIAGHGLFRSEAKVGDTVVVLGTGPIGLFSIQWAKIFGSTKIIAVDVFDEKLDLAKELG
                                                                                                                                                                                                                                                                                                                    ----CDECKKGLYSRCNNVAIIGNKELGGCFAEYTKVKERNLIKIPDEISYETAAALEP
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Plazanet-Menut Claire
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RESULT 5 US-09-908-744-53

Sequence 53, Application US/09908744 Publication No. US20030068791A1

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Application US/09908744 vo. US20030068791A1

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; TYPE: PRT
; ORGANISM: Bacillus halodurans
US-09-908-744-50
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SOFTWARE: PatentIn Ve:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIOR FILING DATE: 2001-01-22

PRIOR APPLICATION NUMBER: US 09/488,581

PRIOR FILING DATE: 2000-01-21

PRIOR APPLICATION NUMBER: US 08/790,585

PRIOR FILING DATE: 1997-01-29

PRIOR APPLICATION NUMBER: US 08/368,395

PRIOR APPLICATION NUMBER: US 08/368,395

PRIOR FILING DATE: 1995-01-03
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URRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: PCT/FI01/00051
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350 HLKDGVEKGFKQLIEHKENNVKILVTPNEVS 380
                                 265 DYQIERFYFEKIVRNELHVYGSWNALSSPFPGKEWATTIHYMSSGQLNV---APMISYRL
                                                                                                             210 ISSLQRPAHKQILEYT-NGIGVDVAVESAGTPSTSAQVFALPKKGGEVVFLGI----PYA
                                                                                                                                                                                       150 AHGFYRTNIKPGASVAIMGVGSIGLLAVQWAKIFGATTVFAIDIDEQKLNVANQLGADVL
                                                                               301 FMPMSLTYQEKYATG--
                                                                                                                                                   241 DPSTCDDANAVLKAMVPENEGFHAAFDCSGVPQTFTTSIVATGPSGIAVNVAVWGDHPIG
                                                                                                                                                                                                                   181 WHAVERARFQPGOTALVLGGGPIGLATILALOGHHAGKIVCSEPALIRRQFAKELGAEVF
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                                                                                                                                                                                                                                                                                                                                                   -KKLGPYVPGMTFGHEFAGEVVKIGRSVTGFSIGDRVAACPTYTC--
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Koivuranta Kari
Londesborough John
Aristidou Aristos
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                                                                         -SMCYTVKDFQEVVKALEDGLISLDKARKMITGKV 349
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Mismatches
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ches 176;
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TYPE: PRT
; ORGANISM: Escherichia coli
US-09-815-242-10187
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10187
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Best Local Similarity
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Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Identification of Essential TITLE OF INVENTION: Prokaryotes
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    327
                                          346
                                                                                                                          286
                                                                                                                                                       213 VRFPVAKELGATAVVNGSTEDVVARCQQICGKDNLGL--VIECSGANIALKQAIEMLRPN
                                                                                                                                                                                                                                       153 AAVLDPICNAYKSIAQQSKFLPGQDVVVIGTGPLGLFSVQMARIMGAVNIVVVGLQEDVA 212
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                                                                                                                                                                                                                                                                             171 GALVEPISVAWHAV-ERARFQPGQTALVLGGGPIGLATILALQGHHAGKIV---CSEPAL 226
                                                                                                                                                                                                                                                                                                                                                             120 GLCMACQSGSPNCCASLSFCGLGGAS--GGFAEY-VVYGE-----DHMVKLPDSIPDDI
                                                                                                                                                                                                                                                                                                                     93 GVCPACEQGDFLCCTEKVNLGLDNNTWGGGFSKYCLVPGEILKIHRHALWEIPDGVDYED 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKGLLYYGTNDIRYSE-TVPEPEIKNPNDVKIKVSYCGICGTDLKEFTYSGGPVFFPKQG
THRIGLSQWRE-GFDAMVD--KTAIKVIMT 353
                                   TGKVHLKDGVEKGFKQLIEHKENNVKILVT 375
                                                                       GEVVRVGM-GFKPLDFSINDITAWNKSIIGHMAYDSTSWRNAIRLLASGAI---KVKPMI
                                                                                                                 GIAVNVAVWGDHPIGFMPMSLTYQEKYATGSMCYTVKDFQEVVKALEDGLISLDKARKMI
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Zyskind, Judith W.
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28.2%;
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; Pred. No. 1.4e-23;
66; Mismatches 162;
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; ORGANISM: Bacillus halodurans (deduced sequence)
US-09-908-744-70
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PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: US 09/488,581
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 08/790,585
PRIOR FILING DATE: 1997-01-29
PRIOR APPLICATION NUMBER: US 08/368,395
PRIOR FILING DATE: 1995-01-03
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Best Local Similarity 28.7%;
Matches 111; Conservative 5
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SEQ ID NO 70
LENGTH: 343
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318 TISEW-DKAYHAI--KSGEAIKVLLTP 341
                                350 HLKDGVEKGFKQLIEHKENNVKILVTP 376
                                                                  261 QVGLFAQPEIQFNFEKIIQKEISVVGSRSQKPADWEPALSLLNEKKVN---AKTLVTHEY 317
                                                                                                      290 NVAVWGDHPIGEMPMSLTYQEKYATGSMCYTVKDEQEVVKALEDGLISLDKARKMITGKV
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                                                                                                                                                                                                                                                                                                                                                                             52 ------VAAPVTLGHEFSGEIVELGEGVTGFNVGDRVTSETTYSIC-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKGLL--YYGTNDIRYSETVPEPEIKNPNDVKIKVSYCGICGTDLKEFTYSGGPVFFPKQ 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/973,325
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                                                                                                                                           KEVGIDY----AIDTQEVDIKELVSELTDGYGADVVLECSGAVPAAKQGIDLLRKKGQYA 260
                                                                                                                                                                                 KELGAEVFDPSTCDDANAVLKAMVPE-NEGFHA--AFDCSGVPQTFTTSIVATGPSGIAV 289
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                                                                                                                                                                                                                     LACTHHAIAKTSINKGDLVVVTGPGPIGL---LAAQVAKSHGGTVIITGLSNDQVRLKKA
                                                                                                                                                                                                                                                ISVAWHAVERARFQPGQTALVLGGGPIGLATILALQ--GHHACKIVCS--EPALIRRQFA 232
                                                                                                                                                                                                                                                                                                --GKCSYCTSGDYNLCSHRK--GLGNQQDGSFAKYVIARQESLHHLPAGVDDRSAAMTEP
                                                                                                                                                                                                                                                                                                                                    DLGLCMACQSGSPNCCASLSFCGLGG-ASGGFAEYVVYGEDHMVKLPDSIPDDIGALVEP 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKALVKTQHGTGHFAVQEK-PEP-TPGKHQVKIKVKYTGVCGSDI--HTYEG---HYP--
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No. US20030068791A1
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US-09-908-744-51
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CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: PCT/FI01/00051
PRIOR FILING DATE: 2001-01-22
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NUMBER OF SEQ ID NOS: 70
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                                                                                                                                                                                                        175 EPISVAWHAVERARFQPGQTALVLGGGPIGLATILALQGHHAGKIVCSEPALIRRQFAKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
mes 112; Conserv
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FILING DATE: 1997-01-29
APPLICATION NUMBER: US 08/368,395
FILING DATE: 1995-01-03
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ISLDKARKMITGKVHLKDGVEKGFKQLIEHKENNVKILVTPNEV 379
                               ----KIGFLGIAYSDITLSEEAFENIFRKELELKGFWNSYSAPFPGQEWTKGINLVNEGK 308
                                                                                                    LGADII--INAKDINPVEKIKELTGGKGVDIALECAGSKITQEQCLLITKKKS-----
                                                                                                                                       LGAEVFDPSTCDDANAVLKAM-VPENEGFHAAFDCSGVPQTFTTSIVATGPSGIAVNVAV
                                                                                                                                                                       EPLAVAMHGVLNIGVQVGDTVAVMGSGTMGQLVIQGLKIAGAGTIIAVDISDNKLRESKE
                                                                      WGDHPIGFMPMS---LTYQEK----
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                                                                  ----YATGSMCYTVKDFQEVVKALEDGL 335
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LENGTH: 343
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APPLICANT: Dartois, Veronique
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CURRENT APPLICATION NUMBER: US/09/922,501
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US 09/633,294
PRIOR FILING DATE: 2000-08-04
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 APPLICANT:
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                                                                             ce 52, Application US/09908744 ation No. US20030068791A1
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                                                               INFORMATION:
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                              Ojamo Heikki
Povelainen Mira
Gros H+kan
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Pred. No. 4.8e-23;
3; Mismatches 149;
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US-09-925-300-1326
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Sequence 1326, Application Patent No. US20020151681A1 GENERAL INFORMATION:

US/09925300

APPLICANT: Craig Rosen, APPLICANT: Steve Ruber

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SEQ ID NO 52
LENGTH: 352
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Best Local Similarity
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PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 08/790,585
PRIOR FILING DATE: 1997-01-29
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PRIOR FILING DATE: 2001-01-22
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PRIOR APPLICATION NUMBER: US 08/110,672
PRIOR FILING DATE: 1993-08-24
PRIOR APPLICATION NUMBER: US 07/973,325
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CURRENT FILING DATE: 2001-07-20
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                                                                                                                                                                                                                                                           180
                                                                  270 -ELPLSADATECILRGELTLKGSWNSYTSPYPGRAWTATLDFMEKGDIIF---KPMISDK 325
                                                                                                                                             215 ILNS--KEVNVIKEIKKITNGGADVVIETAGSRFTQEQSLFVAKKRGNIVFVGI--SHT- 269
                                                                                                                                                                                                                      155
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 326
                                 349 VHLKDGVEKGFKQLIEHKENNVKILV 374
                                                                                                          300 GFMPMS-----
                                                                                                                                                                                240 FDPSTCDDANAVLKAMVPENEGFHAAFDCSGVPQTFTTSIVATGPSGIAVNVAVWGDHPI 299
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                                                                                                                                                                                                                                                       AWHAVERARFQPGQTALVLGGGPIGLATILALQGHHAGKIVCSEPALIRRQFAKELGAEV 239
                                                                                                                                                                                                                                                                                            GKCDYCNEGNFGLCDDYNIIGT-RVNGAFAEYVRVPEEHILKLPDTLDYETAAGIEPATI
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                                                                                                                                                                                                                                                                                                                                                                                                                                             MRASVLYNVGDVRY-EMVDIPEITD-TQVLVNVKYVGICGSDLPRSMVSG------- 52
                                                                                                                                                                                                                      AYHGISKSNIRVGDSVVVLGCGPIGQFVIQWAKVFGASKIIAVDIFDEKLELSKLLGANY 214
IGLNE-VGDFLSKMSKREINFNKILV
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Koivuranta Kari
Londesborough John
Aristidou Aristos
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Plazanet-Menut Claire
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                                                                                                        -LTYQEKYATGSMCYTVKDFQEVVKALEDGLISLDKARKMITGK 348
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Pred. No. 7.6e-23;
   350
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APPLICANT: Kimoto, Hiroaki
APPLICANT: Kimoto, No. US2003032153A11hiro
TITLE OF INVENTION: NOVEL (R) 2, 3-BUTANEDIOL DEHYDROGENASE,
TITLE OF INVENTION: MCTHODS FOR PRODUCING SAME, AND METHODS FOR PRODUCING STILE OF INVENTION: MCTHODS FOR PRODUCING ALCOHOL USING THE DEHYDROGENASE
TITLE OF INVENTION: MCTHODS FOR PRODUCING TITLE OF INVENTION: MCTHODS FOR PRODUCING TITLE OF INVENTION UNMBER: US/10/147,003
CURRENT APPLICATION NUMBER: US/10/147,003
CURRENT FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: JP 2001-159647
PRIOR FILING DATE: 2001-05-28
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 385
TYPE: PRT
RESULT 3
US-09-815-242-11979
; Sequence 11979, Application US/09815242
; Patent No. US20020061569A1
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US-10-147-003-2
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Best Local Similarity
Matches 208; Conserv
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361 QLIEHKENNVKILVTPNEVS 380
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DELMNHKEKNIKILLTPN 376
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                                                                                                                                                                               GFMPMSLTYQEKYATGSMCYTVKDFQEVVKALEDGLISLDKARKMITGKVHLKDGVEKGF 359
                                                                                                                                                                                                                           DPSEHKEDAVNILKKLAPGGEGFDFAYDCSGVKPTFDTGVHATTFRGMYVNIAIWGHKPI
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                                                                                                                                                                                                                                                                                                                                                                                                              VHDVSGLGLPQAMGHEMSGIVSKVGPKVTNIKAGDHVVVEATGTCLDHYTWPNAAHAKDA 118
                                                                                                                                                                                                                                                                                                                                                   ECAACQRGFYNCCAHLGFMGLGVHSGGFAEKVVVSEKHVVKIPNTLPLDVAALVEPISVS
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; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-11979
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PRIOR APPLICATION NUMBER: 05/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
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SOFTWARE: FastSEQ for Windov
SEQ ID NO 11979
LENGTH: 363
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Best Local
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA 011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKGLLYYGTNDIRYSETVPEPEIKNPNDVKIKVSYCGICGTDLKEFTYSGGPVFFPKQGT 60
EELVNNKEHNVKIIVSP 361
                                                                                                                                                                      FDPSTCDDANAVLKAMVPENEGFHAAFDCSGVPQTFTTSIVATGPSGIAVNVAVWGDHPI
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                           **CLIEHKENNVKILVTP 376
                                                                         EFNFFELVSTEKQLLGALAYN-GEFADVIAFIADGRLDI---APLVTGRIGLEEIVERGF
                                                                                                         GFMPMSLTYQEKYATGSMCYTVKDFQEVVKALEDGLISLDKARKMITGKVHLKDGVEKGF
                                                                                                                                            LDPSRC-DALGEIRALT-GGLGADVSFECIGNKHTAKLAIDAIRKAGKCVLVGIF-EEPS
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Pred. No. 1.6e-44;
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11;

RESULT 4
US-09-815-242-11975
; Sequence 11975, Application US/09815242
; Patent No. US20020061569A1

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Title: Perfect score:

OM protein

Scoring table: Sequence:

Minimum DB Maximum DB

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Database :

Sequence 10958, A
Sequence 4, Appli
Sequence 7, Appli
Sequence 12466, A
Sequence 5706, App
Sequence 412, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 10162, A
Sequence 12430, Appli
Sequence 13832, A
Sequence 13832, A
Sequence 13827, Appli
Sequence 1313, Appl
Sequence 81, Appli
Sequence 81, Appli
Sequence 9, Appli
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1: /cgn2_6/ptodata/1/pubpaa/U
2: /cgn2_6/ptodata/1/pubpaa/U
3: /cgn2_6/ptodata/1/pubpaa/U
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2013
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24.092 Million cell updates/sec
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: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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10 US-09-815-242-10187

9 US-09-908-744-70

9 US-09-908-744-51

10 US-09-908-744-52

10 US-09-908-744-52

10 US-09-915-242-5705

10 US-09-815-242-13873

10 US-09-915-242-13873

10 US-09-815-242-13833

10 US-09-815-242-13833

10 US-09-815-242-13833

10 US-09-815-242-13833
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US-10-147-003-2

US-09-815-242-11979

0 US-09-815-242-11975

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US-09-908-744-53

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US-09-908-744-50
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    Sequence 70, Appl
Sequence 51, Appl
Sequence 15, Appl
Sequence 52, Appl
Sequence 5705, Ap
Sequence 1326, Ap
Sequence 13773, A
Sequence 13833, A
Sequence 13833, A
Sequence 421, App
Sequence 421, App
                                                                                                                                                                                                                                                                                    Sequence 2, Appli
Sequence 2, Appli
Sequence 11975, A
Sequence 11975, A
Sequence 50, Appl
Sequence 50, Appl
Sequence 10187, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Tani, Neurola, Neurola Applicant: Tani, Yoshiki
FILE OF INVENTION: NOVEL (R)-2,3-BUTANEDIOL DEHYDROGENASE
FILE REFERENCE: 06501-092001
CURRENT FAPPLICATION NUMBER: US/10/020,674
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: JP 2000-333363
PRIOR FILING DATE: 2000-10-31
NUMBER.OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 380
TYPE: PRI
ORGANISM: Pichia angusta
US-10-020-674-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/10020674
Patent No. US20020160468A1
GENERAL INFORMATION:
APPLICANT: Yamamoto, Hiroaki
APPLICANT: Onodera, Keiko
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US-10-020-674-2
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Best Local Similarity 100.0%;
Matches 380; Conservative 0
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9 US-10-002-245-4
10 US-09-775-009-7
10 US-09-815-242-12466
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10 US-09-738-938-1
10 US-09-738-938-1
10 US-09-947-027-2
10 US-09-915-009-9
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Pred. No. 8.9e-179;
); Mismatches 0;
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Result

Pred. No. score grea

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Score

Indels

0;

Gaps

0;

60

120

240

120 60

2013
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567.5
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357.5
357.5
337.5
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317.5

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CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patentin Ver. 2.0
SQFTWARE: Patentin Ver. 2.0
SQFTWARE: PATENTIN VER. 2.0
CREANISM: Homo sapiens
US-09-925-300-1326
           PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-26
PRIOR PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-09-815-242-5705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5705, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                     FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                      APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                         APPLICANT:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 TALVLGGGPIGLATILALQGHHAGKIVCSEPALIRRQFAKELGAEVFDPSTCDDANAVLK 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 16.2%;
1 Similarity 30.1%;
86; Conservative 4
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Zyskind, Judith W.
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/269,308
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Pred. No. 3.9
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.9e-22;
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; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSEQ for Windows Ver:
; SEQ ID NO 5705
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5705
                                                                          TITLE OF INVENTION: IGNILIANT OF ESS.
FILE REFERENCE: ELITRA.011A.
CURRENT APPLICATION WUMBER: US/09/815,24:
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-21
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PELICATION WHEER: 60/207,727
PRIOR PELICATION WHEER: 60/207,727
PRIOR APPLICATION WUMBER: 60/207,727
PRIOR APPLICATION WUMBER: 60/242,578
PRIOR APPLICATION WUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
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US-09-815-242-12464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 2/...
100; Conservative
                                           PRIOR APPLICATION NUMBER: 60 PRIOR FILING DATE: 2000-12-
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APPLICATION NUMBER: 60/
FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                           Carr, Grant J.
Yamamoto, Robert T.
Xu, H. Howard
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Q for Windows Version
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                     60/269,308
                                                              60/257,931
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; ORGANISM: Staphylococcus aureus
US-09-815-242-12464
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US-09-815-242-13773
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SOFTWARE: FastSEQ for
SEQ ID NO 12464
LENGTH: 354
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                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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OR APPLICATION NUMBER: 60/242,578
OR FILING DATE: 2000-10-23
OR APPLICATION NUMBER: 60/253,625
OR FILING DATE: 2000-11-27
OR APPLICATION NUMBER: 60/257,931
OR FILING DATE: 2000-12-22
OR FILING DATE: 2000-12-26
OR FILING DATE: 2001-02-16
                                                                                                                                                                                                                   ADDITY
                                                                                                                                                 FILING DATE: 2000-03-21
APPLICATION NUMBER: 60/206,848
FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
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Trawick, John D.
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Yamamoto, Robert T.
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Windows Version 4.0
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US-09-815-242-13773
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 13773
LENGTH: 347
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TYPE: PRT
                                                                                                                                               121 LCMACQSGSPNCCASLSFCGLGGASGGFAEYVVYGEDHMVKLPDSIPDDIGALVEPISVA 180
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                                                                                                                                                                             Local Similarity 28.2 es 81; Conservative
                                                                                                                                                                                                                                      1 MKSVVIHAEGDVRVEER-PLPQLQAEDDVLVKVVSSGLCGSDIPRIFAQGAHYY----- 53
                                                                                                                                                                                                                                                                 1 MKGLLYYGTNDIRYSETVPEPEIKNPNDVKIKVSYCGICGTDLKEFTYSGGPVFFPKQGT 60
                                                                                                                                                                                                KDKISGYELPICPGHEFSGTVVEVGSGVTSVKPGDRVAVEATSHCSDRSRYKDTVAQDLG 120
                              DPSTCDDANAV---LKAMVPENEGFHAAFDCSGVPQTFTTSIVATGP 284
                                                          LHAFHLAQGCEGKNVIIVGAGTIGLLALQCARELGARSVTAIDINPQKLELAKALGA---
                                                                                     WHAVERARFOPGOTALVLGGGPIGLATILALQGHHAGKIVCSEPALIRROFAKELGAEVF 240
                                                                                                                  -THTCNSREMTADDIQTALSDIQFDQLVLETAGTPQTVSLAIDITGP 252
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Pred. No. 4.3e-21;
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Search completed: May 2, 2003, 15:32:41 Job time : 1363 secs

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Database
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Listing first 45 s
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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			88848884			
AC095016 AC006225 AE003673 HSU07361 BC025295 AX337243	AX417038 AX417041 AE008841 AX377790 DMAF002212 AC004266 AE001572_0 AC020282	AP001520 AB042810 CER04B5 AR165148 ARF323504 AB016256 AL596165 AP003005	AB015478 AE004831 AY052067 AY058731 AY057946 AE006323 SPTMS1 SPUA1410 SPBC1773	CNSO6K6L AX133848 AF370.161 AY085213 AB025569 AB025569 AE008211 AE009402	SCU12980 CNS06.T04 AX36.6887 AB007638 BSUB0004 AX312470	
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ALIGNMENTS

RESULT 1
SCU12980
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

SCU12980

103682 bp DNA linear PLN 05-MAR-1998
Saccharomyces cerevisiae chromosome I left arm sequence.

V12980 U00091

V12980.1 GI:3911250

S. cerevisiae Ycr28p homolog; FLO9; GDH3; two alcohol/sorbitol dehydrogenase homologs; SIM1; CNE1; ACS1; S.pombe SPAC 1F7.03
homolog; S.cerevisiae Pip2p-like transcription factor homolog; GCV3, glycine cleavage H protein; PTA1; FUN9 transcript, essential gene, S.pombe SPAC 24B11.08c homolog; CDC24; CLN3/WHI1/DAF1; CYC3; PYK1; S.cerevisiae ORF 06283 homolog; CDC24; CLN3/WHI1/DAF1; CYC3; PYK1; S.cerevisiae ORF 06283 homolog; EUN33 transcript, essential gene; FUN9 transcript, essentia

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EMBO J. 7 (13), 4335-4346 (1988)
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Alberghina, L.,
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Volckaert, G. and Valle, G.
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de Virgilio,C., Burckert,N., Neuhaus,J.M., CNEI, a Saccharomyces cerevisiae homologue mammalian calnexin and calreticulin yeast 9 (2), 185-188 (1993)
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Mol. Cell. Biol. 13 (12), 7901-7912 (1993)
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Submitted (27-OCT-1997) Department of Genetics,
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Saccharomyces
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22 (bases 1 to 103682)
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http://genome-www.stanford.edu/
11: yeast-curator@genome.stanford.edu.
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Genomic exploration of the hemiascomycetous yeasts: yeast species for molecular evolution studies FEBS Lett. 487 (1), 3-12 (2000)
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                                                                                              Bolotin-Fukuhara,M., Bon,E., Brottler,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
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/note="similar to Saccharomyces cerevisiae ORF YALO61w
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                             AAGAGCTTTTGTTCAAACTTCCTGATGAATTATCATATGAACAAGGCGCGCTCGTTGAAC
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AB007638
AB007638.1
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                                                                                                                                                                                                                                                                                                                                                                                                Submitted (03-0CT-1997) Yoshito Sadale, National Institute of Genetics, Radioisotope Center; Yata 1111, Mishima, Shizuoka Japan (E-mail:ysadaie@lab.nig.ac.jp, Tel:81-0559-81-6870, Fax:81-0559-81-6870)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kasahara,Y., Nakai,S., Ogasawara,N., Yata,K. and Sadaie,Y. Sequence analysis of the groESL-cotA region of the Bacillus subtilis genome, containing the restriction/modification system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus subtilis (strain:Marburg 168) DNA.
Bacillus subtilis
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(bases 1 to 16585)
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/db_xref="GI:2522012"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transl_table=11
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VERSION
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                                                                                                                                                                                                                                                                                                   DEFINITION
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                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                   AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCACCTCAATTGTCGCCACGGGACCTTCTGGAATCGCCGTCAATGTGGCCGTTTTGGGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACGTACAGGAGGCGGTGTTGACGTAGCATTCGAAGTCACTGGTGTCCCCAGTGGTGTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCGCGATCATCGTTGATCCGTCTAAAACAGACGATGTAGTCGCTG-----AGATTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCGCTGAAGTGTTCGATCCTTCTACATGTGACGACGCAAATGCTGTTCTCAAGGCTATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAACTGATATTTACGCTGTTGAGCTTTCTCCTGAACGCCAGCAAAAAGCTGAGGAGCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGGGCAAAATTGTGTGTTCCGAGCCGGCCTTGATCAGAAGACAGTTTGCAAAGGAACTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTCTGCAGTTGCTCTATACGCTGTCCGCTCAAGCAAACTCAAAGCAGGCGACAAAGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGAGCTTTTGTTCAAAACTTCCTGATGAATTATCATATGAACAAGGCGCGCCTCGTTGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGGATTCCTCGGCTTAGCCGGCGGAGGCGGCGGTTTCTCTGAATACGTCTCTGTGGATG 10047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240;
Carter, N.M., Choi, S.K., Codani, J.J., Connerton, I.F., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Emmerson, P.T., Entian, K.D., Errington, J., Fabret, C., Foulger, D., Fritz, C., Fujita, M., Fujita, Y., Fuma, S.,
                                                                                                                                                                                       Bacillus subtilis. Bacillus subtilis
                                                                                                                                                                                                                                                                                                 Bacillus subtilis complete genome (section 4 of 21): from 600701 to
                                                                       Kunst, F., Ogasawara, N., Moszer, I., Albertini, A.M., Alloni, G., Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Boursiss, R., Boursier, L., Brans, A., Braun, M., Brignell, S.C., Bron, S., Brouillet, S., Bruschi, C.V., Caldwell, B., Capuano, V.,
                                                                                                                                                                                                                                             Z99107 AL009126
Z99107.1 GI:26
                                                                                                                                                                                                                                                                                                                      BSUB0004
                                                                                                                                                                        Bacteria;
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                                                                                                                                                  cteria; Firmicutes; (bases 1 to 213190)
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                                                                                                                                                                                                                                               GI:2632866
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.38;
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                                                                                                                                                                    Bacillales; Bacillaceae; Bacillus
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Pred. No. 5.6e-12;
                                                                                                                                                                                                                                                                                                                      213190 bp
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                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                      BCT 26-NOV-1997
               Ehrlich, S.D.,
Ferrari, E.,
                                                      Cummings, N.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6,
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JOURNAL
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                        gene
        SgS
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Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A.

Direct Submission

Submitted (18-Nov-1997) I. Moszer, A. Danchin, Institut Pasteur,

Regulation de 1'Expression Genetique, 28 rue du Docteur Roux, 75724

Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr,

adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The complete genome sequence of the gram-positive bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Danchin, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Galleron, N., Ghim, S.Y., Glaser, P., Goffeau, A., Golightly, E.J., Grandi, G., Guiseppi, G., Guy, B.J., Haga, K., Halech, J., Harwood, C.R.,
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complement(1199. .1441)
                          /gene="ydgA"
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DFYODEEVHRIIVEMPGVYEEELTIRLLSKYOLLIKGTITPVFPAEMEVLRERYYGEI
ERIIQLPEAAETHILQIQLLNGLLHISYPRQVETVAFNKGL"
                                                                                                                                                                                                                                                                                                                                                                complement (755. .1186)
                                                                                                                                                                                                                                                                                                                                                                                                   complement(755. .1186)
/gene="ydfT"
                                                                                                                                                                                              /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      LESIMRKMRYTLDYLINOOLREKEIFNIEEVLFAILETMGOLTYLRKPOFRHYTKODLM
IAVNOEORLFIELIMDEEIIENNLKONRLTESWLLEELRKRDIKVKETVYAVLLGNGD
IYVDQYKDHISVPMDKE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AIAAGLAYNTSIKPHNMAISFSIFVLTIFLISFLSIKNRKLRKFFAGDPTVLIQNGKI
                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                              /gene="ydfT"
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/db_xref="GI:2632867"
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/translation="MIELEVVIRTVASFGLLLIAERILGKQTISQMTIFDFIAAITLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function="unknown"
/note="similar to hypothetical proteins"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Bacillus subtilis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3117. .3590
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3117. .3590
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Qayenmipngrdssnhyfwnitndggermgwlwlyadplhpqkeafiysfglyeafrg
                                                                    complement(3705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="SPTREMBL:P96699"
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complement(1455. .1727)
/gene="ydgB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MKSKGVBSRKRILKAAANEFSVRGFHDAKVSEIVKKAGFTQPSF
YLYPOSKEAIFAELITDFHSRVRKLTESLILENGLNTEDVSKRVLLAVETVPGFLDED
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                                                                                               /gene="expZ
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                                                                                                                                                                                                                                                                                                                               /transl_table=11
                                                                                                                                                                                                                                                                                                                                                       codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="ydgE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAB12377.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2026. .2613
/gene="ydgC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="SPTREMBL: P96700"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein_id="CAB12378.1"
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/note="similar to hypothetical proteins"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _table=11
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terminator terminator

PAT 14-DEC-2001

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CTGTATTCGGCTGCGGCCCGATCGGACTTCTTGTCATTGAAGCGCTGAAGGCTGCCGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGAGCTTTTGTTCAAACTTCCTGATGAATTATCATATGAACAAGGCGCGCTCGTTGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGAGCTTCTGCGGTTTGGGTGGTGCCAGCGGCGGTTTTGCCCGAGTACGTCGTTTACGGTG
                                                                              CCACCTCAATTGTCGCCACGGGACCTTCTGGAATCGCCGTCAATGTGGCCGTTTGGGGAG
                                                                                                                                                                                                                                                                                                                GCGCTGAAGTGTTCGATCCTTCTACATGTGACGACGCAAATGCTGTTCTCAAGGCTATGG
                                                                                                                                                                                                                                                                                                                                                                          CAACTGATATTTACGCTGTTGAGCTTTCTCCTGAACGCCAGCAAAAAGCTGAGGAGCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGGCAAAATTGTGTGTTCCGAGCCGGCCTTGATCAGAAGACAGTTTGCAAAGGAACTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTCTGCAGTTGCTCTATACGCTGTCCGCTCAAGCAAACTCAAAGCAGGCGACAAAGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTATTTCTGTTGCCTGGCATGCTGTTGAACGCGCTAGATTCCAGCCTGGTCAGACGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGACCACATGGTCAAGCTGCCAGACTCGATTCCCGACGATATTGGAGCACTGGTTGAGC
                           GACAAGCCATCCAGTCCACTACAATTGCCGGTGAAACCGTCATCGTCAGCATTTGGGAAA
                                                                                                                                          AACGTACAGGAGGCGGTGTTGACGTAGCATTCGAAGTCACTGGTGTCCCAGTGGTGTTAC
                                                                                                                                                                                                    TGCCGGAGAACGAGGGATTCCATGCAGCCTTCGACTGCTCTGGTGTTCCTCAGACATTCA
                                                                                                                                                                                                                                                          GCGCGATCATCGTTGATCCGTCTAAAACAGACGATGTAGTCGCTG-----AGATTGCAG
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Yfldeadtkinsledotiliefkonysgymkfrekkrltooreyekookhverieadmu
Glasnsekahaostkkegfkeyhrvkakktdaoikskokrlekelekakaepvipeyt
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/gene="ydgf"
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/db_xref="SWISS-PROT:P39115"
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QYSGTLLAVSHDRYFLEKTTNSKLVISNNGIEKQLNDVPSERNEREELRLKLETERQE
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Pred. No. 7.5e-12;
D; Mismatches 235;
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                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
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                                                            AUTHORS
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                                                                                                                                                                                                                                                                                                                CNS06K6L 717 bp DNA linear T7 end of clone AT0AA002E01 of library AT0AA from T7 end of clone Servazzii, sequence tagged site.
                                                                                                                                                                                                                                     AL402499.1
STS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human polynucleotides and polypeptides Patent: WO 0190366-A 5455 29-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G. Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casarego de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A.,
                                                                                                               Saccharomycetales;
                                                                                                                                                                            Saccharomyces servazzii
                                                                                                                                                                                                       Saccharomyces servazzii.
                                                                                                                                                                                                                                                                                              AL402499
                                                                                                                                                   Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                          (bases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
70 c 101 g 9
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                                                                                                                        Saccharomycetaceae;
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No. 2e-08;
         Brottier,P., Casaregola,
rrens,P., Lepingle,A., Ll
                                                                                                                                                Saccharomycotina;
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                                                                                   241 GTGGTCGAGGTTGGCTCTGGTGTCACAAGTGTGAAACCTGGTGACAGAGTCGCAGTTGAA
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                                GTGAAAGCTATTGGACCAGCCGTGACTCAATTTAAAGTAGGGGACCGAGTCGTCGTCGAA
                                                                                                                                               AGACATAAGCTAAGTGAAAATGAACTTCCCCARGCTCTTGGACACGAGGTRAGTGGTTAT
                                                                                                                                                                                                                                                                                                                ACGGACTTGAAAGAATTCACATATTCTGGAGGTCCTGTTTTTTTCCCTAAACAAGGCACC 180
                                                                                                                                                                                                                                                                                                                                                                         CCAAAGCTTACTTCCCCTGATAGTCTACTTATAAGCCCCTCGTTTGTAGGATTGTGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGGAGATCAAGAATCCCAACGATGTCAAGATCAAAGTCAGCTATTGTGGAATCTGTGGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGAGAGGTTTAGCTTATTTTAAAGAAGGTGATATACATTTCACAGATAGTTTGCCAGAA
                                                                                                                                                                                                                                                              AGTGACTTGCATGAG-----GCAAGCCATCCAATCTTTTTCCCTAAAGATGGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exiguus, Saccharomyces sērvazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: sequencagope.cns.fr - Web: www.genoscope.cns.fr)
This STS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Casaregola, S., Lepingle, A., Bon, E., Neuveglise, C., Nguyen, H., Artiguenave, F., Wincker, P. and Gaillardin, C.
Genomic exploration of the hemiascomycetous yeasts: 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces servazzii FEBS Lett. 487 (1), 47-20584717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genoscope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(<10. .>33)
/note="similar to Saccharomyces cerevisiae ORF YAL060w [
FUN49 ; similarity to alcohol/sorbitol dehydrogenase ]
similar to Saccharomyces cerevisiae ORF YAL061w [ FUN50 ;
similarity to alcohol/sorbitol dehydrogenase ]"
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/strain="CBS 4311"
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/note="end : T7"
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/clone="ATOAA002E01"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL CDNAS: Yamada, K., Chang, C.H., Dale, J.M., Deng, J.M., Hsuan, V.M., Lee, J.M., Quach, H.L., Tang, C.C., Toriumi, M., Wallender, E.K., Wong, C., Wu, H.C., Yu, G., Yuan, S., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (17-JUL-2002) Plant Gene Expression Center, 800 Buchan Street, Albany, CA 94710, USA
The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAs (RAFL CDNA: 'RIKEN Arabidopsis Full-Length CDNA'): Seki,M., Narusaka,M., Ishida, Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 1126)
2 (bases 1 to 1126)
2 (bases 1 to 1126)
2 (manda,K., Chan,M.M., Chang,C.C., Toriumi,M., Wallender,E.K.,
Lee,J.M., Quach,H.L., Tang,C.C., Toriumi,M., Wallender,E.K.,
Wong,C., Wu,H.C., Yu,G., Yuan,S., Bowser,L., Carninci,P., Chen,H.,
Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A.,
Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A.,
Karlin-Neumann,G., Kawai,J., Kim,C.J., Lam,B., Lin,J., Miranda,M.,
Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M.,
Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M.,
Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Deng, J.M., Hsuan, V.W., Lee, J.M., Quach, H.L., Tang, C., Toriumi, M., Wallender, E.K., Wong, C., Wu, H.C., Yu, G., Yuan, S., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Yawai, J., Kim, C., J., Sakurai, T., Satou, M., Seki, M., Shino, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AY133848 1126 bp mRNA linear PLN 07-AUG-200
Arabidopsis thaliana clone U10156 putative sorbitol dehydrogenase
(At5951970) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana. Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                    Yamada,K. (SSP/PGEC) and Sek1, M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis Open Reading Frame (ORF) Clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosidae; eurosids II
1 (bases 1 to 1126)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Theologis,A.
                                                                                                                                                                                                     ecotype: Columbia"
                                                                                                                                                                                                                                /note="This clone
                                                                                                                                                                                                                                                                                     /chromosome="5"
                                                                                                                                                                                                                                                                                                                /organism="Arabidopsis thaliana
/db_xref="taxon:3702"
                          /evidence=experimental
                                                           /codon_start=1
                                                                                   /gene="At5g51970"
                                                                                                                                         /gene="At5g51970"
                                                                                                                                                                                                                                                           /clone="U10156"
'product="putative
                                                                                                                                                                                                                                18
sorbitol dehydrogenase"
                                                                                                                                                                                                                                'n
                                                                                                                                                                                                                                pUNI 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deng, J.M., Hsuan, V.W., Wallender, E.K.,
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800 Buchanan

Ishida,J.,

Lee, J.M.,

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REFERENCE
AUTHORS
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AF370161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 597
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Nobluse, Value, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA, complete cds.
AF370161
AF370161.1 GI:13877796
                                                                                                                                                                                                   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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LAVAKQLGADEIVQVTTNLEDVGSEVEQIQKAMGSNIDVTFDCAGFNKTMSTALAATR
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/db_xref="GI:22136876"
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47.1%;
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                                                                                             Pham, P.K., Banh, J., Chung, M.K.,
H.L., Toriumi, M., Yu, G., Bowser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.4e-07;
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357 TGGGCTCTGTATGGCCTGCCAGAGCGGATCTCCGAACTGCTGTGCGTCGCTGAGCTTCTG 416 TTGGAGATGCAATCTCTGCAGGGAAGGACGATACAACCTTTGTCCAGAAATGAAGTTCTT 438

379

Matches

Conservative

0;

Mismatches

270;

Indels

9;

Gaps

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TITLE
JOURNAL
REFERENCE
                                                                                                   ORIGIN
                                                                                                                            BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAs: Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D., Lee,J.M., Quach,H.L., Tang,C.C., Toriumi,M., Yu,G., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin Neumann,G., Kim,C., Koesema,E., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
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3 (caning, M., Vu, Guach, H.L., Tang, C.C., Toriumi, M., Yu, Goldsmith, A.D., Lee, J.M., Quach, H.L., Tang, C.C., Toriumi, M., Yu, Goldsmith, A.D., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) this work. Shinozaki,K. (RIKEN GSC) and Theo contributed equally to this work as PIs.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (18-APR-2001) Plant Gene Expression Center Street, Albany, CA 94710, USA RIKEN Genomic Sciences Center (GSC) members carried
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K.,
Davis,R.W., Ecker,J.R. and Theologis,A.
Arabidopsis Full Length cDNA Clones
         Similarity
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                                                                                                                               354
                                                                                                                   /gene="At5g51970"
/gene="At5g51970"
/ 218 c 338
                                                                                                                                                                                                                                                                                                                                            RVRMKAVGICGSDVHYLKIMRCADFVVKEPMVIGHECAGIIEEVGEEVKHLVVGDRVALEEE LEPGISCWRCNLCREGRYNLCPEMKFFATPPVHGSLANQVVHPADLCFKLPENVSLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="This clone is in a modified pBluescript vector (Lambda ZAP) as a XhoI/SstI insert. ecotype: Columbia"
                                                                                                                                                                                                                                                         LAVAKQLGADEIVQVTTNLEDVGSEVEQIQKAMGSNIDVTFDCAGFNKTMSTALAATR
CGGKVCLVGMGHGIMTVPLTPAAAREVDVVGVFRYKNTWPLCLEFLTSGKIDVKPLIT
                                                                                                                                                                                                                                                                                                                  GAMCEPLSVGVHACRRAEVGPETNVLVMGAGPIGLVTMLAARAFSVPRIVIVDVDENR
                                                                                                                                                                                                                      HREGESOKEVEDAFETSARGSNAIKVMENL"
                                                                                                                                                                                                                                                                                                                                                                                                                            /product="putative sorbitol dehydrogenase"
/protein_id="AAK43976.1"
/db_xref="GI:13877797"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Arabidopsis
/db_xref="taxon:3702"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="At5g51970"
                                                                                                                                                                                                                                                                                                                                                                                                            translation="MGKGGMSQGEGSKVEEENMAAWLVGINTLKIQPFLLpSVGPHDV/
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   DB 8;
1.4e-07;
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                               Length 1269
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AY085213.1
                                                  wallbu, CA 90265, USA
This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have
                                                                                                                                                                                                                                                                                                                                                                                Genome Biol. (2002) In press 2 (bases 1 to 1347) Brover, V., Troukhan, M., Alexi
frame shifts in a coding region. A sequence is considered to 5'-truncated if it lacks the translation initiation start (A) sequence is considered to be 3'-truncated if it lacks the
                                                                                                                                                                                                                      Submitted (11-MAR-2002) Ceres, Inc,
                                                                                                                                                                                                                                           Feldmann, K.
Direct Submission
                                                                                                                                                                                                                                                                                   Brover, V., Troukhan, M.,
                                                                                                                                                                                                                                                                                                                                            Feldmann, K.
Full-Length cDNA from
                                                                                                                                                                                                                                                                                                                                                                                                                                                   annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1347)
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                (ATG).
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CG-----AGGGATTCCATGCAGCCTTCGACTGCTCTGGTGTTCCTCAGACATTCAC
                                                                                                                                                                                          GATTGTACAAGTGACAACAAACTTAGAGGATGTTGGTTCTGAGGTTGAACAGATTCAGAA
                                                                                                                                                                                                                                        GTTCGATCCTTCTACATGTGACGACGCAAATGCTGTTCTCAAGGCTATGGTGCCGGAGAA
                                                                                                                                                                                                                                                                                          TGTTATTGTGGATGTTGATGAGAACCGTTTAGCCGTAGCAAAACAGCTCGGCGCAGATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="sorbitol dehydrogenase-like protein"
/protein_id="AAM62446.l"
/protein_id="AAM62446.l"
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GAMCEPLSVGVHACRRAEVGPETNVLVMGAGPIGLVTMLAAQAFSVPRIVIVDVDENR
LAVAKQLGADEIVQVTNLEDWGSEVEDIQKANGSNIDVTFDCAGFNKTMSTALAATR
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/db_xref="taxon:3702"
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Prunus persica r complete cds. AB025969

mRNA for

1457 bp mRNA linear PLN 04-AH NAD-dependent sorbitol dehydrogenase,

PLN 04-APR-2000

AB025969

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                                                                                                                                                                                                                   GAGGTCCTATCGGCCTTGCCACCATTCTTGCTCTGCAAGGCCATCATGCGGGGCAAAATTG
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CGGAGAACGAGGGATTCCATGCAGCCTTCGACTGCTCTGGTGTTCCTCAGACATTCACCA 829
                                    TCAAGCTGCCAGACTCGATTCCCGACGATATTGGAGCACTGGTTGAGCCTATTTCTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTTGGGTGGTGCCAGCGGCGGTTTTGCCGAGTACGTCGTTTACGGTGAGGACCACATGG
                                                                                                                TCATTGTGGATGTGGATGAGGGGCTTATCCATTGCAAAGTCTCTCGGCGCCGACGACG
                                                                                                                                                                                              GTGTTCATGCCTGTCGGCGAGCCAACATCGGCCCAGAAACAAATGTCCTGGTGATCGGAG
                                                                                                                                                                                                                                                                                                                 CCTGGCATGCTGTTGAACGCGCTAGATTCCAGCCTGGTCAGACGGCCCTGGTTCTTGGAG
                                                                                                                                                                                                                                                                                                                                                        TCAAGCTCCCGGAGAATGTGAGTTTGGAAGAAGGCGCCATGTGCGAGCCTCTGAGTGTTG
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                                                                         -----TGTTCGATCCTTCTACATGTGACGACGCAAATGCTGTTCTCAAGGCTATGGTGC
                                                                                                                                                     TGTGTTCCGAGCCGGCCTTGATCAGAAGACAGTTTGCAAAGGAACTGGGCGCTGAAG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (08-APR-1999) Kunio Yamada, National Research Institu of Vegetables, Ornamental plants and Tea, Dep. of Floriculture, Lab. of Postharvest Technology; 360 Kusawa, Ano-cho, Age-gun, M 514-2392, Japan (E-mail:yamakuni@nivot.affrc.go.jp, Tel:+81-59-268-4664)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prunus persica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
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NAD-dependent sorbitol dehydrogenase.
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/protein_id="BAA94084.1"
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LEEGAMCEPLSVGVHACRANIGPETNVLVIGAGPIGLVSVLSARAFGAARIVIVDVD
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ATRPGGKVCLVGNGHGVMTVPLTPAAAREVDVVGIFRYKNTMPLCLEFLRTGKIDVKP
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197. .1300
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/db_xref="taxon:3760"
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187 of the complete sequence.
AE008211 AE007870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Agrobacterium tumefaciens str. C58 (Cereon). Agrobacterium tumefaciens str. C58 (Cereon) Bacteria; Proteobacteria; alpha subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Street, Cambridge, MA 02139, USA
Approximately 800 bp of telomeric sequence missing
end of the chromosome and 200 bp missing from the 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (14-AUG-2001) Bioinformatics, Cereon Genomics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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complement(89. .661)
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                                                                                                                                                                                                                                                            complement[942. .1937)
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system, probably ribose specific"
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GLQFGIETVNRYENHLLNSAEQAVALVERIGADNIFIHLDTFHMNMEEKGIANGIIAA
                                   complement(1934
                                                                         MAPLGHGTLLGLPIPLLIFIVCVGIWHVLLTRTKLGFGLLMIGSNIEAARYSGLNTRK
IQVLVYTLSGLMCAVAGIIMLARFNSVRVGHGESYLLITVLAAFLGGINPFGGFGRVL
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                                                                                                                                                                                                                                                                                                                                                             complement (942.
                                                                                                                                                                                                                                                                                                                                                                               WRPVAANTEESLEKGLAFLRDKANQYRIFE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PVFVALIVLQLLSSGLNLLGANQHLATALWGVLMIVVMAARGLFSSYFASLRKKV"
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                                                                                                                                                                                                                                               codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:181661"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Agrobacterium tumefaciens str. C58 (Cereon)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                     .2950)
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the right
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ASSVLSNNRHGAEILTAAILAHAAKGGSLGPDDVILFGGHDDHASRERIDGFHAAKAD
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YFGVEGGDDIEITGYSPHMTEMAFERFFGRRGRLPRGFFVNSSINTEGGLRENGGRHDG
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IPPRTALEGPLDDIWDPVALRRMAK"
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LHNAMADAALAYIKANYPDMKLVGDRYGVAEDLDKSRSTALDLMSANADLKGFLAFGS
QGPIGAGRAVEERRKDGKVFVIGPFSPEQGAKLIKSGALTGGEWMNPKQAGEVFITLA
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complement(2943, .4487)
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6878. .7267
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complement(4551
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ADVVSRWISALGVKIĞLPEDPIRTLSGĞNOORVAIAKMLAIGPKILILDAPTVGVDVG
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system, probably ribose specific"
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                                                                                                                                                                                                                                                                                                                                                              'note="fructose transport system repressor Fruk PA3563
imported] - Pseudomonas aeruginosa (strain PAO1)"
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ORIGIN
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cps

CDS

gene

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Query Match 5.6%;
Best Local Similarity 47.5%;
Matches 225; Conservative
                                                                                                                                                                                                                9832 ACTTGTCAACGAATACAACGTCCAGAAAATTCCGGACGAGATGACCGACGAAGAGGCCGC
576 TCAGACGGCCCTGGTTCTTGGAGGAGGTCCTATCGGCCTTGCCACCATTCTTGCTCTGCA 635
                                                                                                                                                                                                                                                                                                                                                                                           396 CTGTGCGTCGCTGAGCTTCTGCGGTTTGGGTGGTGCCAGCGGCGGTTTTGCCGAGTACGT 455
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                                                                                           ACTGGTGGAACCCTCGGCCGTTGCCGTTTATGCCTGTGATCGCGGTGGCGTTACCGCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EAVIVSETRLREHRQQAEDLLHIARSGLERLYRQVAEQNYVLLLSDRQGVTVEELGDP
SFNNNLRKAGLYLGSEWSEPRAGTCAVGACIATGESLT INGTUHEDVTHTPLSCTAAP
IYDTQGALTAVLDISLLSSPILKTSQNMARHLYSSTVRIE ELANLMASSRHDLYLRFA
GAPEFLDVDPERALSVDGSGRITGMTHAARLLAASRGLDMRWPERLLGORYEEFFEA
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PMLLDRILEKHGMPGRPLTLSNAARLTILHHRWPGNIRELDNAIAFAAALCDDGLITV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INGSWAYPTHYWPRVIRLIASGLLPATKIVTKRITLDTAVTEGFDALLDPAGTHLKIL
IDLSK"
3346 c 3137 g 1989 t
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9311. .10504
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/note="(AE006323) 2,3-butanediol dehydrogenase (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDLPEQLTPASSTPMIDSRGTDLRALLAACNGNISEAARRLGVDRTTLHRRMRRLGIG
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akalmdtrofedaaohloeaironpdysavwaalgecrerlgdhegaaaawiegvava
irrgdioakromevrerrlotrslsas"
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Pseudomonas aeruginosa (strain PA01)"
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Pred. No. 1e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           246;
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                                                                                                                                                                                                                                                                                  FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10072 CCGCAATGTCATCCGTGATGTCATCACCATCAACCCCAAGCGCGATAATGTCGGTGATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9952
                                  CDS
                                                                                                                gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGTCCGCTCGGCAACCGAAGGCAAGGTCGGCTGCGACGTGGCGATCGAATGCGTGGGTAA 10191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTCAAGGCTATGGTGCCGGAGAACGAGGGATTCCATGCAGCCTTCGACTGCTCTGGTGT 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAATAGCGTTCTGGTCACGGGTGCCGGCCCGATCGGCATGTTGACGCTTCTGGCGGCCCG 10011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCTCAGACATTCACCACCTCAATTGTCGCCACGGGACCTTCTGGAATCGCCGT 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---AAAGGAACTGGGCGCTGAAGTGTTCGATCCTTCTACATGTGACGACGCAAATGCTGT 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARUUY402 11742 bp DNA linear BCT 20-DEC-20-Agrobacterium tumefaciens str. C58 linear chromosome, section 172 of 187 of the complete securence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wood, D.W., Setubal, J.C., Kaul, R., Monks, D., Chen, L., Wood, G.E., Chen, Y., Woo, L., Kitajima, J.P., Okura, V.K., Almeida Jr., N.F., Zhou, Y., Bovee Sr., D., Chapman, P., Clendenning, J., Deatherage, G., Gillet, W., Grant, C., Guenthner, D., Kutyavin, T., Levy, R., Li, M., McClelland, E., Palmieri, A., Raymond, C., Rouse, G., Saenphimmachak, C., Wu, Z., Gordon, D., Eisen, J. A., Paulsen, I., Karp, P., Romero, P., Zhang, S., Yoo, H., Tao, Y., Biddle, P., Jung, M., Krespan, W., Perry, M., Gordon-Kamm, B., Liao, L., Kim, S., Hendrick, C., Zhao, Z., Dolan, M., Tingey, S.V., Tomb, J., Gordon, M.P., Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Agrobacterium tumefaciens str. C58 (U. Washington).
Agrobacterium tumefaciens str. C58 (U. Washington)
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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Chen,Y. Woo,L., Kitajima,J.P., Okura,V.K., Almeida Jr.,N.F.,
                                                                                                                                                                                                                                                                                                                                      Submitted (27-SEP-2001) Department of Microbiology, University of Washington, 1959 NE Pacific Ave, Box 357242, Seattle, WA
                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                          and Nester, E.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 294 (5550), 2317-2323 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                  98195-7242, USA
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od, D.W., Setubal, J.
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                                                                                                                                                                                                    Washington)"
'gene="acnB"
                                                      note-"Atu4734"
                                                                                /gene="acnB"
                                                                                                                                                                       /strain="C58"
                                                                                                                                                                                                                        organism="Agrobacterium tumefaciens str.
                                                                                                                                             db_xref="taxon:180835"
                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                                                           .11742
                                                                                                                   .3002
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MGPMLIGIAIILAIAS" 5940. .6569

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/codon_start=1 /transl_table=11 gene

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eronkimelypartdaardlingveveelghovitlmdagkodeaoomalnulrkt
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/gene="Atu4735"
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/gene="Atu4735"
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PQSVKVTFKGTMQPYMDFRDVVHATQAQMLQQHGDNVFQGRIIEVHIGTLLADQAFTF
TDWTAEMKAKASICISEDETLIESLEIAKSRIQIMIDKGMDNAAQTLKGLIDKADQRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FAPNKEISIEGQGLTAVEKIFNRNAVGVTPGKVLHAGSDVRVKVNIVGŠQDTTGLMTA
QELEAMAATVISPLVDGAYQSGCHTASVWDKKAQANTPKLMSFMHNEGVITGRDPKGV
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ALQQQHPDKRYMLLAEKGTMGVGSSBMSGVNNVALMTGKQASPYVPFVNYAPIVAGTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KVLLDVALGNDAAIDAKAGEVLKTQVFLYDADMFRLRDAYKEGSAIARDVLESYAKAE
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located using Blastx/Glimmer"
                                                                                                                                                         KNAAMÝEESTAASHGLAREASSLNRLIAQFKLSEAGYAETAAPMRTASAADRPAVSPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="methyl-accepting chemotaxis
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/noted using Blastx/Glimmer"
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                                                                                                                                                                                                                   VQQGVQLVGETGRALELIVTEVQEINRHVAAISESAQEQSSGLQQINTAVNQMDQDTQ
                                                                                                                                                                                                                                                                                                                  GDFNRAAEQLQSTLTQVAQNARGIDAGANEIRSAADDLARRTEQQAAAVEETAAALEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LATSTRLFQGRVVEDSAEKKGESLLASTPVVVLSAILGRTPSIEEYRSAVEGIDLTKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YYGATKKVDLGFYGSCMVHKGDVKIVAQMLRNMEKTEGKVEFKAPLVVAAPTYNIIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEIRSGETPALKPDANAKYFAEVVVDLDIINEPMIADPDVNNNDVSRRYTHDTIRPVS
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                                                                                                                                                                                                                                                    etafqtnllalnagveaaragdagkgfavvaqevrelaqrsanaaketknlittsngq
                                                                                                                                                                                                                                                                                        ITTTVKDSTKRAQEAGHLVGRAKIGAEKSGEVVQKAVSAMEQIATSANEISNIIGVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
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      ORF located using Glimmer'
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GLDELASLTRSSLPQDRRIVVBDGTVLYAHALEPQDRRSSVPLARRSRPQPVTERIGGD
DENUMNT BEWUTDEVERT GROTT TO THE TOTAL 
                                                GPAVRNLRRKVEKLSPARLPILLQGQTGTGKEHLARIIHDASGVSGRFVAVNCAAIPE
QLIESELFGYLPGAFTGALAKGRKGLVEEAQGGTLFLDEIGDMPFAAQSRLLRVLAEG
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COMPLEMENT (8538...9611)
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RDVITINPKRDNYGDYVRSATEGKYGCDVAIECVGNEHALKACVDAVRKQGVVVQTGL
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TEGFDALLDPAGTHLKILIDLSK"
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/gene="Atu4740"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Atu4741"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="zinc-binding
/protein_id="aAL45534.1
/db_xref="GI:17743246"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mrrpmgaehghdrsrrtwkekreaeaaelgyaegpyyviigggg
ggialgarlrolgyptiiieknerpodswrkrykslolhdpywydhlpyipppenwpy
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/gene="Atu4739"
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RYLLPDEGADRLVIGSFCSIGSGAAFIMAGNGCHRUEWISTFPEFFMDEVPEFENAAN
GYLPAGDTVIGNDVWIGSEAIIMPGITVGDGAVIGTRALVYKDVEPYALVYGGNPAKTI
RKREDDDSIALLLEMKWWGWPAERLKAAMPLWTSGNVAALYRFWRSDSL"
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located using Blastx/Glimmer"
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/protein_id="AAL45533.1"
/db_xref="GI:17743245"
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located using Blastx/Glimmer"
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JOURNAL
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                                                                               Nakamura,Y.

Direct Submission

Direct Submission

Submitted (17-JUN-1998) Yasukazu Nakamura, Kazusa DNA Research

Submitted (17-JUN-1998) Yasukazu Nakamura, Kazusa DNA Research

Institute, Department of Plant Gene Research; 1532-3, Yana,

Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,

Tel:81-438-52-3935, Fax:81-438-52-3934)

Tel:81-438-52-3935, Fax:81-438-52-3934)
Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c-mSG15
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
                                                                                                                                                                                                                                                          Structural analysis of Arabidopsis thaliana chromosome 5. VII. Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned P1 and TAC clones DNA Res. 5 (5), 297-308 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone: MSG15.
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana genomic AB015478 BA000015 AB015478.1 GI:3241926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/Services/MetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
SplicePredictor (Volker Brendel, Stanford University,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://gremlin1.zool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://genome.wustl.edu/eddy/tRNAscan-SE/). This sequence may not be the entire insert of this clone. It may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         r because we remove overlaps between neighboring submissions. clone is MJM18 and the 3' clone is F17P19.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(1. .402)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /profein_id="BAB11042.1"
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KELRQKKTQUKTTRYLPTIRRYLPDGSFEEMGVDELIVEDSWKRQVGGT"
KELRQKKTQUKTTRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRRYLPTIRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVLNLLNETSHTTSRKILTQSIAVLLKSFDVKLEVRMNGGLIFQKVDGPASKGHMKLR
NTNPRDNPSVTFNYYQEPEDLNKCVKGLNTIIRMINSKAFSKYKYPGVTARELLNLML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="mandelonitrile lyase-like protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pir||T05129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAGNOVUTERA
RAGNOVUTERA
DHIYGTKIGGTIFDRAGHRHTAANLLEYANPNRIVYYLHASVHKVLFTTEEKPKAYEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:3702"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Arabidopsis
/strain="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STFLKSPGTNPQATVMMLGR"
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PMVGQGMADNPMNFVAIPSPQPVELSLIQAVGITKFDSYIEGLSGLSLSFDITRRFFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(2611. .3415,4019. .4413,4496.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="gene_i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(6167. .6204,6527. .
7061. .7128,7215. .7284)
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                                                                                                                                                                                                                                                                                                                                                                                          evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               trong similarity to unknown protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ld:MSG15.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thaliana"
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LEPGISCWRCNLCREGRYNLCPEMKFFATPPVHGSLANQVVHPADLCFKLPENVSLEE
GAMCEPLSVGVHACRRAEVGPETNVLVMGAGPIGLVTMLAARAFSVPRIVIVDVDENR
LAVAKQLGADEIVQVTTNLEDVGSEVEQIQKAMGSNIDVTFDCAGFNKTMSTALAATR
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join(12204. .12401,12491. .12604)
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CVEGINTIIKVINSKAFSKFKYPDATIHGLLDLMLSVPTNLRPRHITSMFNLRQFCID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLIQVVGITKFESYIEGASGVIFSYSWTRRFFDGVLNYLNESRTTSTTSPTLSTQSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERGKIFAKQEIRAIQIGPGGIFFTGDGTGQVKVWKWCTEPTAALP Complement(18601. .19275)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MDFDLNGGNKRVENRLGGGGGSTRPMAPTDTRQKVCFHWRAGRC NRSPCPYLHRELPGPGPGQGQGPGYTNKRVALESGFAGPSHRRGPGFNGNSSSSWGRFGGRTTYKTEKVCNFWVDGNCTYGDKCRYLHCWSKGESFALLTQLDGHEKLVSGIALPSGSDKLYTGSKDETLRVWDCASGQCTGVLKLGGEIGCVLSEGGWLLVGMPNLVKAWNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HRFGFSQKEVEDAFETSARGSNAIKVMFNL'
complement(join(15138. .15282,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(20512. .20836,20925.
21377. .21455,21539. .21702,21778. .2
22230. .22312,22406. .22505,22590. .2
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kfretrhpiyrgvrornsgkwycevrepnkkskiwlgtfptvemaarahovaalalrg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVKIWAAIEGGNLEVTYTHKEEHGVLALCGVHDAEAKPVLLCACNDNTLRLYDLPSFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="mgkggmgqgegskveeenmaawlvgintikiqpfilpsvgphdv
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DYVBEQAIWTLSUNAGALEILLUNGSVLWFLIRLUNGSVLWFLRLLYSUNGVLWFLRLLYSUNGVLWFLRLLYSUNGVLWFLRLLYSUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNGVLWFLRLUNG
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VREGERRAEE()NGGVFYMDDEALLGMPNFFENMAEGMLLPPPEVGWNHNDFDGVGDVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="AP2 domain transcription factor-like protein"
/protein_id="BAB11047.1"
/db_xref="GI:10177734"
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/note="contains
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15695. .15814,15916. .16062,16155. .16256,16376. .16465,
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/protein_id="BAB11045.1"
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/db_xref="GI:10177733"
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.21954,22033. .22155,
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QILQLPSPVVLVPALLTIGAMTAGNHQQTQCVINSGALPIISNMLTRNHENKIKKCAC

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RESULT 15
AE004831
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Matches 177
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nes 177; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCTGGACCTATTGCCCTTGTTACAATGTTGGCTGCCTCCGGCTTTCAGTGTGCCTAGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTGTGTTCCGAGCCGGCCTTGATCAGAAGACAGTTTGCAAAGGAACTGGGCGCTGAAGT 716
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   Stover, C.K., Pham, X.Q., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S., Hufnagle, W.O., Kowalik, D.J., Lagrou, Garber, R.L., Goltry, L., Tolentino, E., Westbrock-Wadman, S., Yuan,
                                                                                                                                                                                                       Pseudomonas aeruginosa.
Pseudomonas aeruginosa
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AE004831.1 GI:99
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/note="contains similarity
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wriesclksasssetdmyrnkegifapkekkkvyvlmdldnkpprgppyeaatalrkya
eklgryveisayanrhafillphwyderreerrildemerkgeytpidpyicgykgrk
eklgryveisayanrhafillphwyderreerrenldemerkyptpidpyicgykgrk
ckturldlkhipkqlherrokkyphwrslkgkrqorkeryvsgnekyneaarslltp
kygygleaelrragyyyktyedkpqaadmaykrqiqbbytrgidbulylysddkdfsdm
lrkareadlgtlyvsdmdralgrhadlmypmsgyekgeigekdlipgkrprefeedeyg
                                                                                                             1 to 15088)
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YMAEQSCIKQLCDILVYSDERTTILKCLDGLENMLKAGEAEKNSEDVNPYCLLIEDAE
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/db_xref="GI:10177736"
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                                                                                                                                                                                                                                                                                                       GI:9950347
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Stover, C.K., Pham, X. -Q.T., Erwin, A.L., Mizoguchi, S.D., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D. Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E., Westbrook-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lin, Saith, K.A., S Wong, G.K.-S., Wu, Z., Paulsen, I.T., Reizer, J., Saier, M. Hancock, R.E.W., Lory, S. and Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brody,L.L., Coulter,S.N., Folger,K.R., Kas,A., Larbig,K., Lim,R., Smith,K., Spencer,D., Wong,G.K., Wu,Z. and Paulsen,I.T.
Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
Nature 406 (6799), 959-964 (2000)
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Direct Submission
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/gene="PA4143"
1345. .3504
/gene="PA4143"
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YQQLNGLLFGVENLLYIWLGATMWNDGQFSVGILMAFNAYKSQFDSRVGSLIDKFFEL
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                VLQDDVLFAGSLSDNISFFDPQPDMPWLLQCAQMAAIHDDIQAMPMGYNTLVGDMGTV
                                                                                                                                                                                                                                                                                                                                                                                                              RMLQLQGERLADIVLQAPEVSHGDILPENLREREASIEIQGLRYRYAEQEPWVLDGLD
LRIAGGESVAIVGPSGCGKSTLFNVLLGILPPVEGQIRMAGLDLAQLGLDGLRELVGT
                                                                                                                                                                                                                                                                                                                                                  LSGGQKQRVMLARALYKKPRILFLDEATSHLDVHCEQRVNAAIRALRITRIMVAHRPE
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/protein_id="AAG07530.1"
/db_xref="GI:9950349"
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/strain="PAO1"
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translation="MRALAGLLCGLLGLVPGAAAYEPDVFGTTGQVAGQAVYDLGGSG
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/9 1335
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529.1"
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/gene="PA4148"
8917. .9717
/gene="PA4148"
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TRERDRSIGLQLNIPLFEGFERTYQVRNALARREASEAELADTEQQVSLEVWNNYQSL
SVETRSLARTRELVEQSRQSLEVVQGRYRSGVGSMIELLNALTAYASAEDQHIRALGN
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ASRGYSDMDYNDAPYLSGDGHRHRRGASLQLSWYLFDFGRRSAALRNAQQLLLAANAS
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PASSIAYTLINRLYEAFNPG"
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AFTGAAKCKRGLLQQADGGTLFLDE LGDMPLGLQTRLLRVLABGEVA PLGAARRQAV
DIQVICATHRADLAALVAAGGEREDLY FRLGGARFELPPLRERSDRLALI RRILDEETA
HCGVR I ELGEAALECLLGY RWPGNVRQLRHVLRYACALCGGATLQLADL PAELRGERR
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/gene="acoR"
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FVNGDFTRHLAAFTEEHPDLDLGTACDDSRHDTTGDGTDTAFRTGDLPDSSLKARHLF
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/transl_table=11
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  CAGCTTCGAATGCATCGGCAACAAGCACCGCCAAGCTGGCCATCGATGCCATCCGCAA 14746
                                    AGCCTTCGACTGCTCTGGTGTTCCTCAGACATTCACCACCTCAATTGTCGCCACGGGACC
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IADLEKGMLGANGIVGAGAPLAAGAALAAKLKGSDAVAVAFFCDGGSNEGAVFEAMNL
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/protein_id="AAG07536.1"
/db_xref="GI:9950355"
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/protein_id="AAG07537.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a method for monitoring differential CC expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal CC cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs care used in the methods for monitoring differential expression of genes CC in a first filamentous fungal (FF) cell relative to expression of the CC same genes in one or more second filamentous fungal cells. Monitoring CC the global expression of genes from FF cells allows the production CC potential of the microorganisms to be improved. New genes may be CC identified and gene copy number variation and stability can be CC identified and gene copy number variation and stability can be CC identified and gene copy number variation and stability can be CC identified and gene copy number variation and stability can be CC identified and gene copy number variation and stability can be CC identified and gene copy number variation and stability can be CC identified and gene copy number variation and stability can be CC identified and gene copy number variation and stability can be CC identified and gene copy number variation and stability can be CC identified and gene copy number variation and stability can be CC identified and gene copy number variation and stability can be copy number variation and stability can be cCC analysis, recombination, metabolic or catabolic pathway CCC and charlation of genes can be used to study how FF cells and copy in the c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 536 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAGCGGCGGTTTTGCCGAGTACGTCGTTTACGGTGAGGACCACATGGTCAAGCTGCCAG
                                                 CATGTGACGACGCAAATGCTGTTCTCAAGGCTATGGTGCCGGAGAACGAGGGA 783
                                                                                                       TCAGCTCCAAGAGACGCGAGTTTGCCAAGAAGTTTGGTGCGCATCACGTGTTCGATCCTA
                                                                                                                                  CGGCCTTGATCAGAAGACAGTTTTGCAAAGGAACTGGGCGCTGAAGTGTTCGATCCTTCTA 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGGAGGTTGGCCGAATCAACTGTTGTGCCGCAGGATGCTGTCAAGAAGCTGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGTGCAAGCGCGGCCTTCAGAACTGCTGTGATAAAAAACGGTTTCATCGGGTTGAGTGGCT 133
CAAANGACGATGTCGTGGCGAATGTTGAAAAAATTTGACAGGAGGGCTGGGAA
                                                                                                                                                                                                            GACTGGCTGTTGTGCAGGCTCTCATAGGACGTGGATGCAAGAACATCATGCTGAGCGAGG
                                                                                                                                                                                                                                                          GCCTTGCCACCATTCTTGCTCTGCAAGGCCATCATGCGGGCAAAATTGTGTGTTCCGAGC
                                                                                                                                                                                                                                                                                                                 TCAAGATCTCACCCTACGAGGAAGGCAACTCGGCTTTTGTTGGTGGCGGACCAATTG
                                                                                                                                                                                                                                                                                                                                                                  TTGAACGCGCTAGATTCCAGCCTGGTCAGACGGCCCTGGTTCTTGGAGGAGGTCCTATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTCGATTCCCGACGATATTGGAGCACTGGTTGAGCCTATTTCTGTTGCCTGGCATGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                      ACAATGTGTCCCTAGAAGTCGGCGCTTTAGTCGAACCGCTTGCTGTTGGATGGCACGCAA
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Pred. No. 3.
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RESULT 2 AAD28420

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AAD28420;

AAD28420 standard;

DNA; 1041

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Best Local
                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method for expressing a coding region of interest in a Bacillus sp. The method involves growing a transformed Bacillus sp. having a chimeric gene comprising a nucleic acid fragment comprising the promoter region of a Bacillus gene operably linked to a coding region of interest expressible in Bacillus sp. under oxygen limiting condition, in the presence of nitrate, or in the presence of oxygen at various growth phases. The method is useful for regulating gene expression in Bacillus sp. and for monitoring the cell metabolism of Bacillus sp. culture. The method is useful for monitoring fermentation and regulating bioreactor health. The method is also useful for detecting genotypic alterations amount strains. The genes may be used in modelling systems to test perturbation in fermentation process conditions which will determine the requirements for the high yield of bioprocess production. The present sequence is Bacillus subtilis ydjL gene used in
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1041 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 44; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expression of coding region of interest in a Bacillus species, monitoring fermentation process, involves growing transformed under oxygen depletion, the presence of nitrate or at various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-154741/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                      invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression; cell metabolism; b:
typic alteration; ydjL gene; ds
                                                                                                                                                                                            AAGAGCTTTTGTTCAAACTTCCTGATGAATTATCATATGAACAAGGCGCGCTCGTTGAAC
                                                                                                                                                                                                                          AGGACCACATGGTCAAGCTGCCAGACTCGATTCCCGACGATATTGGAGCACTGGTTGAGC
                                                                                                                                                                                                                                                          TGGGATTCCTCGGCTTAGCCGGCGGAGGCGGCGGTTTCTCTGAATACGTCTCTGTGGATG
CAACTGATATTTACGCTGTTGAGCTTTCTCCTGAACGCCAGCAAAAAGCTGAGGAGCTTG
                          CGGGCAAAATTGTGTGTTCCGAGCCGGCCTTGATCAGAAGACAGTTTGCAAAGGAACTGG
                                                              CTGTATTCGGCTGCGGCCCGATCGGACTTCTTGTCATTGAAGCGCTGAAGGCTGCCGGTG
                                                                                            TGGTTCTTGGAGGAGGTCCTATCGGCCTTGCCACCATTCTTGCTCTGCAAGGCCATCATG
                                                                                                                          CTTCTGCAGTTGCTCTATACGCTGTCCGCTCAAGCAAACTCAAAGCAGGCGACAAAGCGG
                                                                                                                                                          CTATTTCTGTTGCCTGGCATGCTGTTGAACGCGCTAGATTCCAGCCTGGTCAGACGGCCC
                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                          Conservative
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2001US-268320P
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                                                                                                                                                                                                                                                                                                                                                                                      242 T; 0 other
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RESULT 3
ABN777811
ADN ABN777812
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Sequences ABP31028-ABP35561 represent 4534 novel human proteins designated ORF (open reading frame) 1-4534, and sequences ABN75054-ABN79587 represent cDNAs encoding them. The invention also encompasses polypeptides at least 80% identical to the ORF1-ORF4534 (collectively referred to as ORFX) proteins, polynucleotides at least 85% identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX polynucleotides, the recombinant production of ORFX proteins, antibodies specific for ORFX proteins, methods of detecting ORFX polynucleotides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; ORF; open reading frame; ORFX; drug screening; diagnosis; diagnosis; diagnosis; modulation; haematopoiesis regulation; tissue growth; anglogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; cardiovascular disorder; tissue system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic; cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator; cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide; gene; ss.
                                                                                                                                                                                                                                                                                                              Claim 1; Page 1615; 2508pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-MAY-2000; 2000US-206690P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABN77781 standard; cDNA; 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC chemokinetic activity, haemostatic activity, thrombolytic activity, creambound in the determination activity, haemostatic activity, thrombolytic activity, considered and antiinfective activity, and may also be involved in the determination of bodily characteristics, fertility and behaviour. ORFX proteins, convicted acids and antibodies may be used in the treatment of cancers, convicted acids and antibodies may be used in the treatment of cancers, convicted acids and antibodies may be used in the treatment of cancers, convicted acids and antibodies may be used in the treatment of cancers, convicted acids and antibodies may be used in the treatment of cancers, convicted acids and antibodies may be used in the treatment of cancers, convicted acids and antibodies, inmune system disorders, disorders related to organ transphantation, disorders of tissue growth and regeneration, convicted acids and infectious diseases caused by viral, bacterial, convicted acids and other pathogens. ORFX nucleic acids may also be used as a convicted acids may antification and cloning of homologous convicted acids may additionally be used to produce transpenic animals convicted acids may additionally be used to produce transpenic animals convicted acids may additionally be used to produce transpenic animals convicted acids may additionally be used to produce transpenic animals convicted acids may additionally be used to produce transpenic animals convicted acids may additionally be used to produce transpenic animals convicted acids may additionally be used to produce transpenic animals of immunogens to generate specific antibodies, which are useful in the diagnosis, treatment and monitoring of ORFX associated diseases.
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Best Local
          302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 339 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis, treatment and monitoring of ORFX-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell differentiation, immune modulation, haematopolesis regulation, tissue growth, anglogenesis, activin or inhibin activity, chemotactic/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptides, methods of screening for modulators of ORFX expression or activity, and methods of screening individuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide
                                           554 AACGCGCTAGATTCCAGCCTGGTCAGACGGCCCTGGT 590
                                                                                                         242
                                                                                                                                                     494
                                                                                                                                                                                                                                                                                                      122
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                                                                                                                                                                                                      182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 GCTCTGGTGTCACAAGTGTGAAACCTGGTGACAGAGTCGCAGTTGAAGCTACGTCGCATT
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GAGTCTGCGAGTTCAAAGCAGGCTCTACGGCTTTGAT
                                                                                                                                        CGATTCCCGACGATATTGGAGCACTGGTTGAGCCTATTTCTGTTGCCTGGCATGCTGTTG
                                                                                          TCGTGCCCTTAGACGTTGCAGCTTTGATTCAACCGTTGGCTGTGTGCTGGCATGCAATTA
                                                                                                                                                                                                                                     GCGGCGGTTTTGCCGAGTACGTCGTTTACGGTGAGGACCACATGGTCAAGCTGCCAGACT
                                                                                                                                                                                                                                                                                         GCAAAAAGGGCTACTATAACATTTGTTCATATTTGGGGCCTTTGTGGTGCGGGTGTGCAGA
                                                                                                                                                                                                                                                                                                                        GCCAGAGCGGATCTCCGAACTGCTGTGGGTGGTGGTGGTGGTGGTGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTCCGACAGATCGCGCTACAAGGACACGGTCGCCCAAGACCTTGGGCCTCTGTATGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCCTGGTGTGAAAACTTGAAAGTGGGAGACAAGGTAGTTGTCGAGCCCACAGGTACAT
                                                                                                                                                                                         GCGGTGGATTTGCAGAACGTGTTGTGATGAACGAATCTCACTGCTACAAAGTACCGGACT
                                                                                                                                                                                                                                                                                                                                                                                        GCAGAGACCGGTATCGTTGGCCCCTGTCGCCAAACGTTGACAAGGAATGGTGCGCTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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Pred. No. 6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 24; Length 339;
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RESULT 4
AAC49213
 OS X K W X E X D X A C X I D
Arabidopsis thaliana
                        Hybridisation assay; genetic mapping; gene expression protein identification; signal transduction pathway;
                  metabolic
                                                          Arabidopsis thaliana
                                                                              18-OCT-2000
                                                                                                 AAC49213;
                                                                                                                 AAC49213 standard;
                pathway;
                                                                             (first
                 promoter;
                                                                                                                   DNA;
                                                                          entry)
                                                      DNA fragment SEQ ID
                                                                                                                   1113
                                                                                                                   ВP
                 termination
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NO: 60340

control;

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18-JUN-1999; 22-JUN-1999; 23-JUN-1999; 23-JUN-1999; 23-JUN-1999; 23-JUN-1999; 23-JUN-1999; 24-JUN-1999; 28-JUN-1999; 29-JUN-1999; 30-JUN-1999;	14 - MAY - 1999 14 - MAY - 1999 14 - MAY - 1999 14 - MAY - 1999 18 - MAY - 1999 19 - MAY - 1999 20 - MAY - 1999 21 - MAY - 1999 22 - MAY - 1999 25 - MAY - 1999 27 - MAY - 1999 01 - JUN - 1999 01 - JUN - 1999 01 - JUN - 1999 10 - JUN - 1999 10 - JUN - 1999 11 - JUN - 1999 11 - JUN - 1999 12 - JUN - 1999 13 - JUN - 1999 14 - JUN - 1999 15 - JUN - 1999 16 - JUN - 1999 17 - JUN - 1999 18 - JUN - 1999 19 - JUN - 1999 10 - JUN - 1999 10 - JUN - 1999 11 - JUN - 1999 11 - JUN - 1999 12 - JUN - 1999 13 - JUN - 1999 14 - JUN - 1999 15 - JUN - 1999 16 - JUN - 1999 17 - JUN - 1999 17 - JUN - 1999 18 - JUN - 1999 19 - JUN - 1999 19 - JUN - 1999 10 - JUN - 1999 10 - JUN - 1999 11 - JUN - 1999 11 - JUN - 1999 12 - JUN - 1999 13 - JUN - 1999 14 - JUN - 1999 15 - JUN - 1999 16 - JUN - 1999 17 - JUN - 1999 17 - JUN - 1999 18 - JUN - 1999 19 - JUN - 1999 10 - JUN - 1999 10 - JUN - 1999 11 - JUN - 1999 11 - JUN - 1999 12 - JUN - 1999 13 - JUN - 1999 14 - JUN - 1999 15 - JUN - 1999 16 - JUN - 1999 17 - JUN - 1999 18 - JUN - 1999 19 - JUN - 1999 10 - J	EP1033405-A2. 06-SEP-2000; 25-FEB-1999; 05-MAR-1999; 05-MAR-1999; 23-MAR-1999; 24-MAR-1999; 16-APR-1999; 16-APR-1999; 17-APR-1999; 23-APR-1999; 23-APR-1999; 24-APR-1999; 25-APR-1999; 26-APR-1999; 27-APR-1999; 28-APR-1999; 29-APR-1999; 20-APR-1999; 2
99US-0139456. 99US-0139458. 99US-0139459. 99US-0139459. 99US-0139461. 99US-0139462. 99US-0139760. 99US-0139817. 99US-0139817. 99US-014053. 99US-014053. 99US-014053. 99US-014053. 99US-014053. 99US-014053.	99US-0134218 99US-0134217 99US-0134271 99US-0134271 99US-0134271 99US-0134941 99US-0135124 99US-0135629 99US-0136021 99US-0136021 99US-0136792 99US-0137722 99US-0137722 99US-0137724 99US-0137724 99US-0138447 99US-0139452 99US-0139453 99US-0139453	2000EP-0301439. 99US-0123180. 99US-0125788. 99US-0125788. 99US-0126264. 99US-0126264. 99US-0127462. 99US-0128234. 99US-0130077. 99US-0130510. 99US-0130449. 99US-0132048. 99US-0132484. 99US-0132486. 99US-0132486. 99US-0132486.
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	23-JUL-19 26-JUL-19 27-JUL-19 27-JUL-19 27-JUL-19 28-JUL-19 28-JUL-19 28-JUL-19 02-AUG-19 02-AUG-19 04-AUG-19 04-AUG-19 04-AUG-19 05-AUG-19 06-AUG-19 06-AUG-19 11-AUG-12 11-AUG-12 11-AUG-12 11-AUG-12	01-JUL 01-JUL 06-JUL 08-JUL 13-JUL 11-JUL 11-JUL 11-JUL 119-JU
		99US-0141842. 99US-0142154. 99US-0142390. 99US-0142970. 99US-0143542. 99US-0144086. 99US-0144331. 99US-0144331. 99US-0144333. 99US-0144333. 99US-0144333. 99US-0144334. 99US-014435. 99US-014435. 99US-014435. 99US-014435. 99US-014435. 99US-014435. 99US-014435. 99US-014508. 99US-014508. 99US-014508. 99US-014508. 99US-014508. 99US-014508. 99US-0145145.

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Query Match
Best Local S
Matches 248
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20-SEP-1999
21-SEP-1999
23-SEP-1999
24-SEP-1999
29-SEP-1999
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06-OCT-1999
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                                         GTTCGATCCTTCTACATGTGACGACGCAAATGCTGTTCTCAAGGCTATGGTGCCGGAGAA
    GATTGTACAAGTGACAACAACTTAGAGGATGTTGGTTCTGAGGTTGAACAGATTCAGAA
                                                                                  TGTTATTGTGGATGTTGATGAGAACCGTTTAGCCGTAGCAAAACAGCTCGGCGCAGATGA
                                                                                                     TGTGTGTTCCGAGCCGGCCTTGATCAGAAGGAACAGTTTGCAAAGGAACTGGGCGCTGAAGT
                                                                                                                                                          TGCCTGGCATGCTGTTGAACGCGCTAGATTCCAGGCTGGTCAGACGCCCTGGTTCTTGG
                                                                                                                                                                                                                                                                                                                     GGTCAAGCTGCCAGACTCGGATTCCCGACGATATTGGAGCACTGGTTGAGCCTATTTCTGT
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990S-0160981.
990S-01610981.
990S-0161404.
990S-0161406.
990S-0161359.
990S-0161361.
990S-0161361.
990S-0161920.
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99US-0160814.
99US-0160815.
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99US-0159584.
99US-0160741.
99US-0160767.
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99US-0157117.
99US-0157717.
99US-0157763.
99US-0157865.
99US-0158232.
99US-0158232.
99US-0158294.
99US-0159294.
99US-0159295.
99US-0159295.
99US-0159333.
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Pred. No. 8.2e-10;
0; Mismatches 270;
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  RESULT 5
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05-MAR-1999

09-MAR-1999

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29-MAR-1999

01-APR-1999

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08-APR-1999
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23-APR-1999;
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21-APR-1999;
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CACCTCAATTGTCGCCACGGGACCTTCTGGAATCGCCGTCAATGTGG
                                                                     CG-----AGGGATTCCATGCAGCCTTCGACTGCTCTGGTGTTCCTCAGACATTCAC
                                                     AGCTATGGGGTCAAACATCGATGTAACATTCGACTGTGCGGGTTTTAACAAAACCATGTC
871
                           874
                                                        824
                                                                                 827
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss. AAC49216 standard; DNA; 1316 Arabidopsis thaliana. Arabidopsis thaliana DNA fragment SEQ (first entry) ВP Ĥ õ 60351.

2000EP-0301439 99US-0125788 99US-0126785 99US-0126785 99US-0128714 99US-0130449 99US-0130510 99US-0130409 99US-0130409 99US-0131449 99US-0132486 99US-0132486 99US-0132486 99US-0132486 99US-0132486 99US-0134218 99US-0134219 99US-0135629 99US-0137528 99US-0137528 99US-0137528 99US-0137528

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9908-0139462

9908-0139763

9908-0140853

9908-0140853

9908-0141287

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                20
                                          Query Match 5.9%;
Best Local Similarity 47.4%;
Matches 200; Conservative
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11-AUG-1999;
12-AUG-1999;
13-AUG-1999;
13-AUG-1999;
16-AUG-1999;
17-AUG-1999;
18-AUG-1999;
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23-AUG-1999;
23-AUG-1999;
25-AUG-1999;
    357 TGGGCTCTGTATGGCCTGCCAGAGCGGATCTCCGAACTGCTGTGCGTGGGCTGAGCTTCTG 416
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990S-0148171
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990S-0161361
                                           Score 67; DB 21; Length 13
Pred. No. 9e-10;
0; Mismatches 222; Indels
                                                                     Length 1316;
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16-JÜN-1999;
18-JÜN-1999;
19-JÜN-1999;
19-JÜN-1999;
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RESULT 6
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05-MAR-1999
09-MAR-1999
23-MAR-1999
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01-APR-1999
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05-MAY-1999
05-MAY-1999
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99US-012548

99US-0125788

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99US-0126765

99US-0127462

99US-0127462

99US-0128714

99US-012845

99US-0130677

99US-0130677

99US-0130691

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99US-0132486

99US-0132486
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99US-0132487
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99US-0144384
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28-JUL-1999 02-AUG-1999

99US-014

45919

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99US-0145192. 99US-0145145. 99US-0145218.

990S-01. 990S-01. 990S-01.

0146388

46389

99US-01 99US-01 99US-01 99US-01 99US-01

16-AUG

990S-01 990S-01 990S-01

148684 149368 149175

149426 149722

49723

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L3-AUG

99US-01. 99US-01. 99US-01.

48565

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-0148171 -0148319 99US-01

20-AUG

23 - AUG

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Best Local Similarity
Matches 248; Conserv
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22-OCT-1999

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28-OCT-1999;
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                                       Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
EP1033405-A2
                    Arabidopsis thaliana.
                                                                                      Arabidopsis thaliana DNA fragment SEQ ID NO: 60359
                                                                                                            18-OCT-2000
                                                                                                                                  AAC49218;
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99US-0161920.
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99US-0161993.
99US-0161993.
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3-SEP-1999 5-SEP-1999 6-SEP-1999

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25 -MAR -1 01 -APR -1 06 -APR -1 16 -APR -1 19 -APR -1 23 -APR -1 23 -APR -1 23 -APR -1 23 -APR -1 24 -APR -1 26 -APR -1 27 -APR -1 28 -APR -1 29 -APR -1 20 -APR -1 21 -APR -1 21 -APR -1 22 -APR -1 23 -APR -1 24 -APR -1 25 -APR -1 26 -APR -1 27 -APR -1 28 -APR -1 29 -APR -1 21 -APR -1 21 -APR -1 22 -APR -1 23 -APR -1 24 -APR -1 25 -APR -1 26 -APR -1 27 -APR -1 28 -APR -1 29 -APR -1 21 -APR -1 21 -APR -1 22 -APR -1 23 -JUN -1 23 -JUN -1 24 -JUN -1 25 -APR -1 27 -JUN -1 28 -JUN -1 29 -JUN -1 29 -JUN -1 21 -JUN -1 21 -JUN -1 21 -JUN -1 22 -JUN -1 23 -JUN -1 24 -JUN -1 25 -JUN -1 26 -JUN -1 27 -JUN -1 28 -JUN -1 29 -JUN -1 29 -JUN -1 30 -JUN -1	06-SI 25-FI 25-FI 09-M
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16-JUL-1999 99US-01 19-JUL-1999 99US-01 19-JUL-1999 99US-01 19-JUL-1999 99US-01 19-JUL-1999 99US-01 19-JUL-1999 99US-01 19-JUL-1999 99US-01 20-JUL-1999 99US-01 21-JUL-1999 99US-01 21-JUL-1999 99US-01 22-JUL-1999 99US-01 22-JUL-1999 99US-01 22-JUL-1999 99US-01 23-JUL-1999 99US-01 23-JUL	02-JUL-1999; 99US-01 06-JUL-1999; 99US-01 08-JUL-1999; 99US-01 09-JUL-1999; 99US-01 12-JUL-1999; 99US-01 13-JUL-1999; 99US-01 14-JUL-1999; 99US-01 15-JUL-1999; 99US-01
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Query Match 5.9%;
Best Local Similarity 47.1%;
Matches 248; Conservative
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29-OCT-1999;
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23-SEP-1999;
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21-OCT-1999
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                                                              GTTCGATCCTTCTACATGTGACGACGCAAATGCTGTTCTCAAGGCTATGGTGCCGGAGAA
                                                                                                             TGTTATTGTGGATGTTGATGAGAACCGTTTAGCCGTAGCAAAACAGCTCGGCGCAGATGA
                                                                                                                                 TGTGTGTTTCCGAGCCGGCCTTGATCAGAAGGAACTTTGCAAAGGAACTGGGCGCTGAAGT
                                                                                                                                                                                     TGCCTGGCATGCTGTAGACGCGCTAGATTCCAGCCTGGTCAGACGCCCTGGTTCTTGG
                                                                                                                                                                                                                                                                                                                                          CGGTTTGGGTGGCGACGGCGGGGTTTTTGCCCGAGTACGTCGTTTACGGTGAGGACCACAT
                                       GATTGTACAAGTGACAACAAACTTAGAGGATGTTGGTTCTGAGGTTGAACAGATTCAGAA
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990S-0160768.
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99US-0159584.
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99US-0157117.
99US-0157753.
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99US-0155486.
99US-0155659.
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99US-0158029
-AGGGATTCCATGCAGCCTTCGACTGCTCTGGTGTTCCTCAGACATTCAC
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S-0158369
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Pred. No. 9.1e-10;
0; Mismatches 270;
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RESULT 8

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XXX Hybrit KW Proto KW
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28-MAY-1999

01-JUN-1999

03-JUN-1999

04-JUN-1999

07-JUN-1999

08-JUN-1999

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14-JUN-1999
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21-MAY-1999;
24-MAY-1999;
25-MAY-1999;
27-MAY-1999;
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05-MAY-1999;
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11-MAY-1999;
14-MAY-1999;
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05-MAR-1999;
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23-MAR-1999;
25-MAR-1999;
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18-MAY-1999;
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14-MAY-1999;
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28-APR-1999;
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16-APR-1999;
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01-APR-1999;
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99US-0127462
99US-012845
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99US-0132487
99US-0134218
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Best Local Similarity 47.1%;
Matches 248; Conservative
                                                                    14-OCT 1999
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530 TIGGAGATGCAATCTCTGCAGGGAAGGACGATACAACCTTTGTCCAGAAATGAAGTTCTT 589
           357 TGGGCTCTGTATGGCCTGCCAGAGCGGATCTCCGAACTGCTGTGCGTCGCTGAGCTTCTG 416
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9903-0159189
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Pred. No. 9.3e-10;
0; Mismatches 270;
                                                Length 1413;
                                 Indels
                                 9;
                                 Gaps
                                 1;
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16-JUN 1999
17-JUN 1999
18-JUN 1999
18-JUN

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99US-014328

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RESULT 9
AAC38499
ID AAC38499
ID AAC38499
ID AAC3
AXX AAA3
XXX AAAA
XXX BYDT
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                                                                                                                                                                                                                                                                         25-FEB-2000;
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                                                 GTTCGATCCTTCTACATGTGACGACGCAAATGCTGTTCTCAAGGCTATGGTGCCGGAGAA
                                                                                            TGTGTGTTCCGAGCCGGCCTTGATCAGAAGACAGTTTGCAAAGGAACTGGGCGCTGAAGT
                                                                                                                                                                                               CTTCAAATTGCCTGAGAATGTGAGGTTTGGAGGAAGGAGCAATGTGTGAACCACTTAGTGT
                                                                                                                                                                                                           GGTCAAGCTGCCAGACTCGATTCCCGACGATATTGGAGCACTGGTTGAGCCTATTTCTGT
                                                                                                                                                                                                                                       TGCAACTCCACCGGTTCATGGCTCTTTAGCTAACCAGGTGGTTCATCCTGCGGATCTATG
                  CG-----AGGGATTCCATGCAGCCTTCGACTGCTCTGGTGTTCCTCAGACATTCAC
                                      GATTGTACAAGTGACAACAAACTTAGAGGATGTTGGTTCTGAGGTTGAACAGATTCAGAA
                                                                                                                              AGGAGGTCCTATCGGCCTTGCCACCATTCTTGCTCTGCAAGGCCATCATGCGGGCAAAAT
AGCTATGGGGTCAAACATCGATGTAACATTCGACTGTGCGGGTTTTAACAAAACCATGTC
                                                                            TGTTATTGTGGATGTTGATGAGAACCGTTTAGCCGTAGCAAAACAGCTCGGCGCAGATGA
                                                                                                                   AGCTGGACCTATTGGCCTTGTTACAATGTTGGCCTGCGCGCTTTCAGTGTGCCTAGAAT
                                                                                                                                                                       TGCCTGGCATGCTGTTGAACGCGCTAGATTCCAGCCTGGTCAGACGGCCCTGGTTCTTGG
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99US-0161992.
99US-0161993.
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99US-0161360.
99US-0161361.
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99US-0158029
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Pred. No. 2.9e-09;
0; Mismatches 271;
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RESULT 1
AAS54244
                    The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are CC escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets CC for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. CC and to obtain antibodies capable of binding to the expressed proteins. CC The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acids sequence is also useful to screen core for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an CC wide variety of organisms. The present sequence encodes an CC Note: The sequence data for this patent did not form part CC format directly from WIPO at CC format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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                                                                                                                                                                                                                                                                                                                                 Claim 27;
                                                                                                                                                                                                                                                                                                                                                              New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids {\bf r}
                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-611495/70.
P-PSDB; AAU36385.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa DNA
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23-MAY-2000;
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22-DEC-2000;
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23-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         828 CACCTCAATTGTCGCCACGGGACCTTCTGGAATCGCCGTCAATGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                      k R,
                                                                                                                                                                                                                                                                                                                                 Seq ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 2000US-191078P.
; 2000US-206848P.
; 2000US-207727P.
; 2000US-242578P.
; 2000US-253625P.
; 2000US-257931P.
; 2001US-269308P.
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Xu HH;
                                                                                                                                                                                                                                                                                                                                No 7881; 511pp; English.
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Query Match
Best Local Similarity
Matches 326; Conserv

Conservative

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Score 63.8; DB 23; Pred. No. 7.8e-09; 0; Mismatches 357;

5.6%;

Sequence 1092 BP;

191 A; 380 C; 352 G; 169 T; 0

other;

Length Indels

1092; 18;

Gaps

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RESULF 12
ABL03803
ID ABL03
XX ABL03
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  23-MAR-2000;
11-JUL-2000;
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                                                                                   23-MAR-2001; 2001WO-US09231
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                                                                                                                                                                                                                                                                                                                  pharmaceutical;
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                                                                                                                                                                                                                                                                                                                                                                                                  melanogaster expressed
                                                                                                                                                                                                                                                                                                                                            developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
2000US-191637P
2000US-0614150
                                                                                                                                                                                                                                                                                                                                            biology;
                                                                                                                                                                                                                                                                                                                                                                                                     polynucleotide SEQ
                                                                                                                                                                                                                                                                                                                                               cell
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Best Local Sir
Matches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                        Drosophila melanogaster
                                                  pharmaceutical;
                                                               Drosophila;
                                                                                         Drosophila
                                                                                                                     26-MAR-2002
                                                                                                                                                                            ABL07985 standard; cDNA; 1338
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                                                                                                                                                                                                                                                                                                                                                                                     GAACGCGCTAGATTCCAGCCTGGTCAGACGGCCCTGGTTCTTGGAGGAGGTCCTATCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                CACGTCACCATGGAGGAGGGCGCCCTGCTCGAGCCTCTGTGTGGGGCGTGCATGCCTGC
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                                                                                                                                                                                                                                                                         GCCTTGATCAGAAGACAGTTTGCAAAGGAACTGGGCGC 710
                                                                                                                                                                                                                                                                                                                    CTTGCCACCATTCTTGCTCTGCAAGGCCATCATGCGGGCAAAATTGTGTGTTCCGAGCCG
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                                                                                         melanogaster expressed polynucleotide SEQ
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                                                                                                                     (first entry)
                                                  gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319 A; 364 C; 367 G; 294 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.5%;
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                                                                biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    detection reagent for detecting for elucidating cell signalling
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Pred. No. 1.8e
0; Mismatches
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les 172;
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Matches 166
                     15-NOV-2001
                                                         AAH43317 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 18437; 21pp +
                                                                                                         664
                                                                                                                                                                                    544
                                                                                                                                                                                                                                                                                                                                                                             Sequence 1338 BP;
                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid
genes from Drosophila and
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                                                                                                                                                                                                                                                                                                               372 CTGCCAGAGCGGATCTCCGAACTGCTGTGCGTCGCTGAGCTTCTGCGGTTTGGGTGGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PEKE )
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11-JUL-2000;
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   aestivum
                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences.
                                                                                                      GGTGCAGCAGCGTTTGGATGTTGCCAAGGAGCTGGGCGC
                                                                                                                       GGCCTTGATCAGAAGACAGTTTGCAAAGGAACTGGGCGC 710
                                                                                                                                       TTTGGTCACCCTGCTGCCTGCCCAAGCTATGGGTGCATCCGAGATCCTTATCACCGATCT
                                                                                                                                                          CCTTGCCACCATTCTTGCTCTGCAAGGCCATCATGCGGGCAAAATTGTGTGTTCCGAGCC
                                                                                                                                                                             CCGTCGCGCAGGAGTCGGTCTGGGCTCAAAGGTGCTCATTCTGGGCGCGCTGGTCCAATTGG
                                                                                                                                                                                             TGAACGCGCTAGATTCCAGCCTGGTCAGACGGCCCTGGTTCTTGGAGGAGGAGGTCCTATCGG
                                                                                                                                                                                                                  TCACGTCAGCATGGAGGAAGGAGCTCTGCTGGAGCCCCTGTCCGTGGGAGTTCACGCCTG
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                                                                                                                                                                                                                                                                          CAGCGGCGGTTTTGCCGAGTACGTCGTTTACGGTGAGGACCACATGGTCAAGCTGCCAGA
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DB; ABB63882.
                                                                                                                                                                                                                                                                                                                                                5.4%;
Similarity 49.0%;
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orbitol dehydrogenase cDNA
                   (first entry)
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2000US-0614150.
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2.7e-08;
hes 173;
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P-PSDB; AAB47474.
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                                                                                                                                                                                             Conservative
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The sequences given in AAH43311-17 encode enzymes which were used for comparison in the isolation of proteins having aldehyde reductase activity. The isolated aldehyde reductase sequences were identified based on Clustal alignment method. The aldehyde reductase cDNA, operatively linked to a plant specific promoter, is useful for altering the level of expression of aldehyde reductase in a transformed host cell. The aldehyde reductase is also useful in studies facilitating better understanding of carbohydrate metabolism and function in plants, for providing genetic tools for the manipulation the sorbitol biosynthetic pathway, and for providing means to contrarbon partitioning in plant cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 933 BP; 159 A; 277 C; 350 G; 147 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid sequence encoding a polypeptide having aldehyde reductase activity, useful for transforming plants with altered levels of expression of sorbitol biosynthetic enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Column 53-54; 33pp; English.
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CCGGCCCGATCGGCCTGGTCACCATGCTCTCGGCGCCCTTCGGGGCGCCAGGATCG
                                             GAGGTCCTATCGGCCTTGCCACCATTCTTGCTCTGCAAGGCCATCATGCGGGCAAAATTG
                                                                                                      GGGTGCACGCCTGCCGAGCCGACGTGGGCGCGGAGAAGAGCGTGCTCATCATGGGCG
                                                                                                                                                      CCTGGCATGCTGTTGAACGCGCTAGATTCCAGCCTGGTCAGACGGCCCTGGTTCTTGGAG
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                                                                                                                                                                                                            TCAAGCTTCCAGACAACGTGAGCCTGGAGGAGGGCGCCATGTGCGAGCCCCTGAGCGTGG
                                                                                                                                                                                                                                                                                                                  CCACCCCACCTTACCATGGATCACTTGCCGACCAGATTGTGCATCCAGGTGACCTGTGCT
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/note= "No stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
29..931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 57.4; DB 22
Pred. No. 6.6e-07;
0; Mismatches 191
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Best Local Similarity 48.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Listeria innocua
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                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New genomic sequences from Listeria species, useful treatment and prevention of infection, also related antibodies and modulators
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Search completed: May 2, 2003, 08:24:55
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ALIGNMENTS

AUTHORS TITLE	JOURNAL MEDLINE PUBMED REFERENCE	TITLE	REFERENCE AUTHORS	VERSION KEYWORDS SOURCE ORGANISM	CNS0778D LOCUS DEFINITION ACCESSION
Blandin, G., Llorente, B., Malpertuy, A., Wincker, P., Artiguenave, F. and Dujon, B. Genomic exploration of the hemiascomycetous yeasts: 13. Pichia angusta	FEBS Lett. 487 (1), 3-12 (2000) 20584711 11152876 2 (bases 1 to 1057)	Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregoia,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Pichia. 1 (bases 1 to 1057) Souciet, J.L., Aigle, M., Artiquenave, F., Blandin, G.	AL432371.1 GT:12215785 GSS. Pichia angusta. 1 Pichia angusta	CNS0778D 1057 bp DNA linear GSS 08-JUL-2001 T3 end of clone BB0AA009H12 of library BB0AA from strain CBS 4732 of Pichia angusta, genomic survey sequence.

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Direct Submission

Direct Submission

Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:
3 regrefagenoscope.cns.fr - Web: www.genoscope.cns.fr)

seqrefagenoscope.cns.fr - Web: www.genoscope.cns.fr)

rhis GSS is part of a random genomic sequencing program of thirteen
ryeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces

saccharomyces kluyveri, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
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sequence and for the sequence of
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Genoscope.
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20584723
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/strain="CBS 4732"
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Souciet, J.L., Algle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
Bolotin-Fukuhara, M., Bon, E., Durrens, P., Lepingle, A., Llorente, B
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O.,
                                                                                                                                                                                                                                                                                                 Bolotin-Fukuhara,M., Toffano-Nioche,C., Artiguenave,F., Duchateau-Nguyen,G., Lemaire,M., Marmeisse,R., Montrocher,R., Robert,C., Termier,M., Wincker,P. and Wesolowski-Louvel,M. Genomic exploration of the hemiascomycetous yeasts: 11. Kluyveromyces lactis
FEBS Lett. 487 (1), 66-70 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetaceae; Kluyveromyces.
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqrefégenoscope.cns.fr - Web: www.genoscope.cns.fr). This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxil, exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxil, Saccharomyces saccharomyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
                                                                                                                                                                                                                                                                                     FEBS Lett.
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Best Local Similarity
Matches 417; Conserv
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TITLE
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Direct Submission

Library Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic Inserts of 3 to kever prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

Location/Qualifiers
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FEBS Lett. 487 (1), 61-65 (2)
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Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular explution studies
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Bolotin-Fukuhara, M., Bon, E., Brottler, P., Casaregola, S.,
de-Montigny, J., Duljon, B., Durrens, P., Lepingle, A., Llocente, B.,
Malpertuy, A., Neuvegilse, C., Ozier-Kalogeropoulos, O., Potier, S.
Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
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Kluyveromyces thermotolerans
Eukaryota; Fungl; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
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               Conservative
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/note="end: T3"

complement(<45. >883)

complement(55. >883)

/note="similar to Saccharomyces cerevisiae ORF YALO60w [FUN49; similarity to alcohol/sorbitol dehydrogenase]

putative frameshift(s)

similarity to alcohol/sorbitol dehydrogenase]

similarity to alcohol/sorbitol dehydrogenase]"

/...***Complement**

/...**Complement**

// **Complement**

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/strain="CBS 6340"
/db_xref="taxon:4916"
/clone="AYOAAO14D05"
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240 c    218 g    260 t
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Score 233.4; | Pred. No. 3.2e | 1; Mismatches
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AL402690.1
        Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetaceae; Saccharomyces.
                                  Saccharomyces servazzii.
Saccharomyces servazzii
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AUTHORS
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CTGTTACAAGATCCCAAACCATATCCCACTAGAAGTAGTCGCTTTAATCCAACCTATTGC
                                                 CATGGTCAAGCTGCCAGACTCGATTCCCGACGATATTGGAGCACTGGTTGAGCCTATTTC 533
                                                                                                                                                            CTGCGGTTTGGGTGGTGCCAGCGGCGGTTTTGCCGAGTACGTCGTTTACGGTGAGGACCA
                                                                                                                                                                                                                   CAAACCAAAATGCCCAGCATGTAAAAAGGGAATGTACAATACTTGTGCCTACTTGGGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: segref@genoscope.cns.fr - Web: www.genoscope.cns.fr) rhis GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii, exiguus, Saccharomyces servazii, Zygosaccharomyces rouxiis saccharomyces kluyveromyces marxianus var. marxianus, pichia angusta, Debaryomyces hansenii var. hansenii, pichia sorbitophila, angusta, Debaryomyces hansenii var. hansenii, pichia sorbitophila,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEBS Lett.
20584717
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/strain="CBS 4311"
/db_xref="taxon:27293"
/clone="ATOAA004A07"
/clone_1lb="ATOAA"
/note="end: T7"
/2...967
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Casaregola,S., L
Artiguenave,F., '
                                                                             Souclet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                     GSS.
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Eukaryota; Fungi; Ascomycota; Saccharos
Saccharomycetales; Saccharomycetaceae;
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   Lepingle, A., Wincker, P.
   and Gaillardin,C.
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                  Nguyen, H.,
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2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqref@genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces servazzil, Zygosaccharomyces rouxil, Saccharomyces servazzil, Zygosaccharomyces rouxil, Saccharomyces kluyverin, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichila angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and varrowla lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                       TAAAWWACCTGATTTCTTACCTATGGATGTTGGTGCTTTAGTGGAGCCATTGTCTGTTGC
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FEBS Lett. 487 (1), 47-51 (2000)
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/clone="Af70AA011E11"
/clone_11b="Af70AA"
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Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
Belotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
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Kluyveromyces thermotolerans.
Elukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
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2 rue Gaston Cremieux, (
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TGGCACGCGGTCCGCATTTCGAAGCTACAACCAGGTCAGACCGCTTTGGTTTTGGGTGCT
                                         TGGCATGCTGTTGAACGCGCTAGATTCCAGCCTGGTCAGACGGCCCTGGTTCTTGGAGGA
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This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
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/note="similar to Saccharomyces cerevisiae ORF YAL061w [
FUN50 ; similarity to alcohol/sorbitol dehydrogenase ]"
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/note="similar to Saccharomyces cerevisiae ORF YAL060w [
FUN49 ; similarity to alcohol/sorbitol dehydrogenase ]"
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/strain="CBS 6340"
/db_xref="taxon:4916"
/clone="AYOAAOO3AO3"
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Saccharomycetales; Saccharomycetaceae; Kluyveromyces.

1 (bases 1 to 923)
Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Liorente, B.,
Malpertuy, A., Neuvegilse, C., Ozler-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies

EEBS Lett. 487 (1), 3-12 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqrefégenoscope.cns.fr - Web: www.genoscope.cns.fr) This GSS is part of a random genomic sequencing program of thirteen yeast species; Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces Servazzii, Zygosaccharomyces rouxii, seccharomyces Saccharomyces servazzii, Zygosaccharomyces rouxii actionyces Saccharomyces Saccharomyces Saccharomyces Saccharomyces Servazzii, Zygosaccharomyces Saccharomyces Saccharom
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/Variety="lactis"
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                                        TGGGTTGGGCATTATAATGGCTTTGCAACACTTTGGGTGCACTGATATCGTGGTTTCGGA
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RESULT 8 CNS07443 LOCUS

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DEFINITION l (bases 1 to 908)
Soutiet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier Kluyveromyces lactis. Kluyveromyces lactis Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch Saccharomycetales; Saccharomycetaceae; Kluyveromyces, 908 bp clone BAOABO25B04 of library BAOAB Kluyveromyces lactis, genomic surve AL42B329 AL428329.1 GI:13449456 survey DNA line sequence linear rain CLIB Saccharomycetes; GSS 210 07-JUL-2001 of

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This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
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Bolotin-Fukuhara,M., McMarmeisse,R., Montrocher,R.,
Buchateau-Nguyen,G., Lemaire,M., Marmeisse,R., Montrocher,R.,
Robert,C., Termier,M., Wincker,P. and Wesolowski-Louvel,M.
Genomic exploration of the hemiascomycetous yeasts: 11.
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Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
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exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
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                                                                                                                                                                                                                  Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr) seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr) This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces yeast species: Saccharomyces bayanus var.
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Saccharomycetals; Saccharomycetaceae; Pichia.

1 (bases 1 to 1045)
Souclet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
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                                                                                                                                                           Pichia angusta.
Pichia angusta
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
earcharomycetales; Saccharomycetaceae; Pichia
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nilarity 53.8%;
Conservative
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/note="similar to Saccharomyces cerevisiae ORF YAL060w [
FUN49; similarity to alcohol/sorbitol dehydrogenase ]
similar to Saccharomyces cerevisiae ORF YAL061w [ FUN50;
similarity to alcohol/sorbitol dehydrogenase ] "
/evidence=not_experimental
a 239 c 139 g 254 t 2 others
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/db_xref="taxon:4911"
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Pred. No. 1.7e-20;
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                               AUTHORS
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Best Local Similarity
Matches 137; Conserv
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PUBMED
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2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE: (B-mail:
5 seqref@enoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces surveri, Kluyveromyces, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                   AGGCAAAGTCCACCTAAAGGACGGAGTCGAGAAGGGCTTTAAACAGCTGATCGAGCACAA 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAAGTKTCGGGCCTTGGAAGATGTCTCATATCTTTG--ACAAGCGCGCAAGATATTWAC 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTTGTCAAGGCCTTGGAAGATGGTCTCATATCTTTGGACAAAGCGCGCGAAGATGATTAC 1037
                                                                                                                                                                                                                                                                                                              GGAAACCAATGTCAAGATCCTGGTGACTCCGAACGAGGTGTCCTA 868
                                                                                                                                                                               CNSO6L9E 982 bp DNA linear GSS 17-JUT7 end of clone ATOAAO11F10 of 11brary ATOAA from strain CBS of Saccharomyces servazzii, genomic survey sequence.
                         1 (bases 1 to 982)
Souciet, J.L., Aigle
                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
         Bolotin-Fukuhara
                                                                                             Saccharomyces servazzii
                                                                                                                 Saccharomyces servazzii.
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Blandin, G., Llorente
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/note="similar to Saccharomyces cerevisiae ORF YALO60w [FUN49; similarity to alcohol/sorbitol dehydrogenase]"
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/clone="BBOAA005F01"
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/strain="CBS 4732"
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                       Aigle, M.,
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     Bon, E.,
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Pred. No. 2.
                   Artiguenave, F.,
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 Brottier, P.,
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2.8e-18;
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                     Blandin, G
Casaregola, S.,
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                                             242
                                                                                                                                 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqref@genoscope.cns.fr) This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowla lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                     CCTTCTA----CATGTGACGACGCAAATGCTGTTCTCAAGGCTATGGTGCCGGAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                TCAGAACCAGCCAAAAWGAGAAGAGATCTAGCAGAAAAGATGGGATGCCGTGTCTTCGAT
TACACCGTCAAGGACTTCCAGGAAGTTGTCAAGGCCTTGGAAGATGGTCTCATATCTTTG
                                                                                                                                                                                                                   GACGGGTTCGACTACTCGTTCGACTGTTCAGGTGTTCCAGCCACTCTTAGAGCTTCCATC
                                             GTCGATTTCTTCCCAATGGATATCACAAAACAAGAAAAGACTTACACCGGGTCCATGTGT
                                                                                 ATTGGATTCATGCCAATGTCTCTGACTTACCAGGAGAAATACGCTACCGGCTCCATGTGC 954
                                                                                                                               GTCGCCACGGGACCTTCTGGAATCGCCGTCAATGTGGCCGTTTGGG----GAGACCACCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       256;
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Direct Submission
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/strain="CBS 4311"
/db_xref="taxon:27293"
/clone="ATQAA011E10"
/clone_1b="ATQAA0"
/note="end : T7"
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FUN50 ; similarity to alcohol/sorbitol dehydrogenase ]"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
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This GSS is part of a random genomic sequencing program of thirteen this GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zyosaccharomyces rouxii, exiguus, Saccharomyces servazzii, Zyosaccharomyces rouxii, exigus, Saccharomyces kluyveromyces thermotolerans, Kluyveromyces saccharomyces kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
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/clone="xBD0AA002D06"
/clone_lib="xBD0AA"
                                                   /note="similar to Saccharomyces cerevisiae ORF YAL061w [FUN50; similarity to alcohol/sorbitol dehydrogenase]"
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  /evidence=not_experimental
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489 bp DNA linear GSS 01-APR-2004474.dhz90f10.sl Saccharomyces unisporus NRRL Y-1556 Saccharomyces unisporus genomic clone 474.dhz90f10.sl, DNA sequence.
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Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                 AL696793
AL696793 NAP1 Anopheles
                                                                             African malaria mosquito
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Box 832, 4566 Scott Ave., St. Louis
Tel: 314 362 735
Fax: 314 362 7855
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Cliften, P.F., Hillier, L.W., Fulton, L., Graves, T., Miner, T., Gish, W.R., Waterston, R.H. and Johnston, M.
Surveying Saccharomyces genomes to identify functional elements by comparative DNA sequence analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 8.3%;
Similarity 52.0%;
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Contact: Johnston M
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random plasmid subclone.
Location/Qualifiers
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/note="Random genomic sequence"
86 c 116 g 138 t
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/Strain="NRRL Y-1556 (CBS 398)"
/db_xref="taxon:27294"
/clone="474_dhz90f10.s1"
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Meyerhofstrasse 1, 69117 Heidelberg,
Tel: +49 6221 387-440
Fax: +49 6221 387-306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Christophides GK Fotis C. Kafatos laboratory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: christop@embl-heidelberg.de plate: P46 row: B column: 01.
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                                                                                                   596 bp mRNA linear EST 12-DEC-2001 Lf74 near-ripe peach fruit cDNA library Prunus persica cDNA clone Lf74 similar to sorbitol dehydrogenase (AB016256), mRNA sequence. BF717166
Prunus persica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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6, 791-806.
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Pred. No. 1.3e-11;
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Matches 173;
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TCATTGTGGATGTGGATGATGAGCGCTTATCCATTGCAAAGTCTCTCGGCGCCGACG
                                                                TGTGTTCCGAGCCGGCCTTGATCAGAAGACAGTTTGCAAAGGAACTGGGCGCTGAAG 715
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Callahan, A.M., Richie, A.J.,
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primer: M13 Reverse.
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/tlssue_type="Whole fruit minus the stone"
/dev_stage="21-60 Newtons flesh resistance"
/note="vector: Lambda vector UniZap XR; Site_1: EcoRI;
/note="vector: Lambda vector UniZap XR; Site_1: EcoRI;
/note-"vector: Lambda vector UniZap XR; Site_1: EcoRI;
/note-"vector: Lambda vector UniZap XR; Site_1: EcoRI;
/note-"vector: Lambda vector UniZap XR; Note: Lambda vector 
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/cultivar="Loring"
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Search completed: May Job time : 1626 secs 2 2003, 09:32:06

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1: /cgn2_6/ptodata/1,

2: /cgn2_6/ptodata/1,

3: /cgn2_6/ptodata/1,

4: /cgn2_6/ptodata/1,

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Gapop 10.0 , Gapext 1.0
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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3505.315 Million cell updates/sec
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                            US-09-347-803-21
US-09-134-001C-537
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US-09-347-803-1
US-08-466-548B-1
US-08-466-548B-1
US-08-466-71-1
US-08-174-467-1
US-08-452-071-1
US-08-452-071-1
US-08-452-071-1
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US-08-466-1
US-08-474-933-1
US-08-474-67-1
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US-08-174-467-20
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US-08-174-174-17-17-17-17-20
US-09-615-192A-112
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                  Sequence 21, Appl Sequence 19, Appl Sequence 1, Appli Sequence 1, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 19, Appli Sequence 19, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequ
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Patent No. 6274379

GENERAL INFORMATION:

APPLICANT: Famodu, Layo O.

APPLICANT: Kinney, Tony
APPLICANT: Kinney, Tony
APPLICANT: MOZOCO, Buddy
ITITLE OF INVENTION: Plant Sorbitol Biosynthetic Enz
FILE REFERENCE: BB-1176

CURRENT APPLICATION NUMBER: US/09/347,803

CURRENT FILING DATE: 1999-07-02

EARLIER APPLICATION NUMBER: 60/092,952

MUMBER OF SEQ ID NOS: 27

SOFTMARE: Microsoft Office 97

LENGTH: 933

TYPPE: NAME
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; TYPE: DNA
; ORGANIZM: Triticum aestivum
US-09-347-803-21
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US-09-347-803-21
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Best Local Similarity 47.4%;
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TCATCGCCGACGTCGACGACCACCGCCTCTCCGTGGCCAAGTCCCTCGGCGCGGACGCCG
                                                                                                  GAGGTCCTATCGGCCTTGCCACCATTCTTGCTCTGCAAGGCCATCATGCGGGCAAAATTG
                                    TGTGTTCCGAGCCGGCCTTGATCAGAAGACAGTTTGCAAAGGAACTGGGCCGCTGAAGTGT 718
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US-09-615-192A-30
US-09-372-422A-29
US-08-456-200B-16
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US-08-08-195-39-8
US-09-030-270A-8
US-09-030-870-8
US-09-03-87-9
US-08-676-967-2
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US-08-149-097D-23
US-08-487-23
US-08-4894-386-23
US-08-480-386-23
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Pred. No. 1.9e
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RESULT 2
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SEQ ID NO 537
LENGTH: 1065
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-537
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS.
FILE REFERENCE: GTC.O. NUMBER. 115 / 104 / 134 .001C
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Best Local Similarity
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PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
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CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
               GENERAL INFORMATION:
APPLICANT: Famodu, Layo O.
APPLICANT: Hitz, Bill
                                                                Sequence 19, Application US/09347803 Patent No. 6274379
APPLICANT: Kinney,
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                                                                                                                                                                         CGTCCACGTGGTACTGCTGTCATCGTATCAATCTTCGGTCATCCC
                                                                                                                                                                                                                                               GATGTGTCATTTGAAGTTGCTGGTGTAGGTATTACTTTACAACAATCTATTGAAGTAACA
                                                                                                                                                                                                                                                                             CATGCAGCCTTCGACTGCTCTGGTGTTCCTCAGACATTCACCACCTCAATTGTCGCCACG 846
                                                                                                                                                                                                           GGACCTTCTGGAATCGCCGTCAATGTGGCCGTTTGGGGAGACCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
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                                                                                                                                                                                       825
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; TYPE: DNA; ORGANISM: Glycine max US-09-347-803-19
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US-08-466-548B-1
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LENGTH: 1610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08466548B Patent No. 6022712
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Orozco, Buddy
TITLE OF INVENTION: Plant Sorbitol Biosynthetic Enzymes
FILE REFERENCE: BB-1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,952
EARLIER FILING DATE: JULY 15, 1998
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/347,803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ABOUT LAORTORIES
ABOUT PARK ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           503 ACGATATTGGAGCACTGGTTGAGCCTATTTCTGTTGCCTGGCATGCTGTTGAACGCGCTA 562
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                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       683
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                                                   CLASSIFICATION: 435
PATOR APPLICATION DATA:
APPLICATION UNMBER: US 07/998,226
FILLING DATE: 30-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       667
                 FILING DATE: 30-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: WALSH, ANDREA C
                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                 STREET: ONE ABBOTT PARK CITY: ABBOTT PARK
                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                  FILING DATE:
REGISTRATION
                                                                                                                                  APPLICATION NUMBER:
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     NUMBER:
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                                                                                                                                        US/08/466,548E
     34988
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Pred. No. 1.4e-05;
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                                                                                                                                                                           Version
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US-07-998-226F-1
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                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/998,226F
FILING DATE: 30-DEC-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
RAME: WALSH, ANDREA C
REGISTRATION NUMBER: 34988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-466-548B-1
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Best Local 9
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                                                                                                                                                 REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                       TOPOLOGY: linea.
MOLECULE TYPE: DN.
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Schopp, cynthia w
TITLE OF INVENTION: ENHANCED YEAST EXPRESSION USING
TITLE OF INVENTION: REGULATORY CONTROL SEQUENCES FROM YEAST SORBITOL
TITLE OF INVENTION: DEHYDROGENASE GENE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: sarthy, aparna v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
ORGANISM: SACCHAROMYCES CEREVISIAE
STRAIN: 800B
                                                                                                   LENGTH: 2774 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ZIP: 60064-3500
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STREET: ONE ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: ILLINOIS
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MOLECULE TYPE: DN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 72.68;
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TOPOLOGY: linear
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                                                                                     linear
SACCHAROMYCES CEREVISIAE
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                                                                  DNA (genomic)
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PCT-US93-12560-1
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                                     Query Match
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application PC/TUS9312560 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/
FILING DATE: 30-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: WALSH, ANDREA C
REGISTRATION NUMBER: 34988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                 HYPOTHETICAL: NC
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2774 base pairs
TYPE: nucleic acid
                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: DOUDY COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-D
SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LAORTORIES
STREET: ONE ABBOTT PARK ROAD
CITY: ABBOTT PARK
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      Local Similarity 72.
                                                                                                                     STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                             NAME/KEY:
                                                                                                                                        ORGANISM:
                                                                                                                                                                                                                      STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/
FILING DATE: 22-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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788..1856
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                  4.18;
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72.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                    US 07/998,226
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                                                                                                                                                                                                                                                                                                            34988
Score 47.2; DB 5;
Pred. No. 7.2e-05;
0; Mismatches 23;
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Pred. No. 7.2e-05;
0; .Mismatches 23;
                           Length 2774;
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Matches

Indels

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Gaps

APPLICANT:

BOUDET, ALAIN M.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: CDNA US-08-174-467-18
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                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                       RESULT 8
US-08-452-071-18
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Patent No. 545151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local s
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Sequence 18, Application US/08452071 Patent No. 6066780 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/874,166
FILING DATE: 27-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REGISTRATION NUMBER: 95563/PS36.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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INFORMATION FOR SEQ ID NO: 18:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/174,467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SCHUCH, WOLFGANG W.
TITLE OF INVENTION: MODIFICATI
TITLE OF INVENTION: PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280. GGTGACAGAGTCGCAGTTGAAGCT 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1393 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: WASHINGTON STATE: D.C.
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CLASSIFICATION: CLASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20005
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                                                                                                                                                                                                                                                                                                                      268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 67.7 es 63; Conservative
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                                                                                                                                                                                                                                                                                                                   AGTGTGAAACCTGGTGACAGAGTCGCAGTTGAA 300
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Pred. No. 0.00024;
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Best Local Similarity 67.7%;
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1393 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 27-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: Datentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                               GENERAL INFORMATION:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
                                                                                                                                            APPLICANT: BOUDET, ALAIN M.
APPLICANT: INZE, DIRK G.
APPLICANT: SCHUCH, WOLFGANG W.
TITLE OF INVENTION: MODIFICATI
TITLE OF INVENTION: PLANTS
                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                            268 AGTGTGAAACCTGGTGACAGAGTCGCAGTTGAA 300
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                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                             332 AAATTCAAAGTTGGGGACACAGTTGGAGTTGGA 364
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/452,071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE:
                                                CITY: WASHINGTON STATE: D.C.
                                  COUNTRY:
                                                                                   STREET:
                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                 17, Application US/08174467
.. 5451514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCHUCH, WOLFGANG W.
VENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
VENTION: PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                   E: CUSHMAN, DARBY & CU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202-822-0944
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                                                                                                                                                                 MODIFICATION OF LIGNIN SYNTHESIS IN
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                                                                                                      DARBY & CUSHMAN
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Pred. No.
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Score 43.4; DB 3; Pred. No. 0.0008; 0; Mismatches 31;

Length 1419; Indels

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Gaps

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0S-08-452-071-17
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CLASSIFICATION: 800

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,166

FILING DATE: 27-APR-1992

ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 15,773
REFERENCE/DOCKET NUMBER: 95563/PS3

TELECOMMUNICATION INFORMATION:
"FIEPHONE: 202-861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 60.,
The 62; Conservative
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TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 27-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               quence 17, Application US/08452071
tent No. 6066780
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SCHUCH, WOLFGANG W.
TITLE OF INVENTION: MODIFICATI
TITLE OF INVENTION: PLANTS
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                           NAME: KOKULIS, PAUL REGISTRATION NUMBER:
                                                                                                                             CLASSIFICATION:
                                                                                                                                                 FILING DATE:
                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                       STREET: 1100 NEW CITY: WASHINGTON STATE: D.C.
                                                                                                                                                                                                                                                                                                       COUNTRY:
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                        20005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INZE, DIRK G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BOUDET, ALAIN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.25
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M PC compati
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                                                                                                                                                                                                                                                                                                                                                                                                                                    MODIFICATION OF LIGNIN SYNTHESIS IN
                                                                                         US 07/874,166
                                                                                                                                                            US/08/452,071
                         16,773
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Pred. No. 0.0008;
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RESULT 12
US-08-174-467-19
; Sequence 19, Application US/08174467
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US-09-347-803-15
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US-09-347-803-15
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Plant Sorbitol Biosynthetic Enzymes FILE REFERENCE: BB-1176 CURRENT APPLICATION NUMBER: US/09/347,803 CURRENT FILING DATE: 1999-07-02 EARLIER APPLICATION NUMBER: 60/092,952 EARLIER FILING DATE: July 15, 1998 NUMBER OF SEQ ID NOS: 27 SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
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APPLICANT: Hitz, Bill
APPLICANT: Kinney, Tony
APPLICANT: Orozco, Buddy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 95563/PS36321/US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-82-0944
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1419 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                       561
                                                                                                                                                                                                                                                                        495
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                                                                                                                                                                   621
                                                                                                                                                                                                                                                                                                                            435 CGGCGGTTTTGCCGAGTACGTCGTTTACGGTGAGGACCACATGGTCAAGCTGCCAGACTC 494
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                                                                                                                                                                                                                                                                                                        501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: S1
TOPOLOGY: linear
MOLECULE TYPE: CDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268 AGTGTGAAACCTGGTGACAGAGTCGCAGTTGAA 300
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                                                                                                                                                        CCGCGCGGGGGTGGGCCCGAGACGGGCGTGCTCGTGGTGGGCGCCGGCCCCATCGGCCT
                                                                                           GGTGTCGCTGCTAGCGGCGCGAGCC 705
                                                                                                                                                                                         ACGCGCTAGATTCCAGCCTGGTCAGACGGCCCTGGTTCTTGGAGGAGGTCCTATCGGCCT
                                                                                                                                                                                                                          GGTGAGCCTGGAGGAGGGCGCCATGTGCGAGCCGCTGAGCGTGGGCGTGCACGCGTGCCG
                                                                                                                                                                                                                                                       GATTCCCGACGATATTGGAGCACTGGTTGAGCCTATTTCTGTTGCCTGGCATGCTGTTGA 554
                                                                                                                                                                                                                                                                                            CGGCTCGCTGGCGAACCAGGTGGTGCACCCGGCCGACCTGTGCTTCAAGCTCCCCGACGG 560
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62; Conserv
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Score 41.8; DB 4 Pred. No. 0.0023; 0; Mismatches 10

DB 4;

Length 1154; Indels

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Gaps

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ENERAL INFORMATION:

BOUDET, ALAIN M.

MODIFICATION OF LIGNIN SYNTHESIS

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; MOLECULE TYPE: cDNA US-08-174-467-19
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Best Local Similarity
Matches 61; Conserv
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Patent No. 6066780
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,166
FILING DATE: 27-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 19:
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TITLE OF INVENTION: PLANTS
TITLE OF INVENTION: 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1283 base pairs
                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                          TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS TITLE OF INVENTION: PLANTS
                                                                                                                                                                                   APPLICANT:
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                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                    276
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                                                                                                                                                                   APPLICANT:
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STRANDEDNESS: 51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 955
LECOMMUNICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/174,467 FILING DATE: 28-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: .nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                      TCCTATGGTCCCTGGCCATGAAGTGGTTGGTGAGGTTGTTGAGGTGGGATCAGATGTGAC 275
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                                    WASHINGTON
D.C.
                                                                                                                                                                                                                                                         Application US/08452071
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                                                                                                                                                                                   BOUDET, ALAIN
INZE, DIRK G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202-861-3000
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Pred. No. 0.
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0.006;
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US-08-125-468-1/c
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Best Local S
Matches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5589385
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENCTH: 1283 base pair
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: TEM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
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ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 27-APR-1992
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                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,468
FILING DATE: 22-SEP-1993
                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 TCCTATGGTCCCTGGCCATGAAGTGGTTGGTGAGGTTGTTGAGGTGGGATCAGATGTGAC 275
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Tsevdos, Estelle J
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                       ITLE OF INVENTION:
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les 61; Conserv
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                                                                                                                                                                                              COUNTRY: US
ZIP: 07470
                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGGTTCAAAGTTGGAGATGTTGTCGGTGTTGGAG 310
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). 5589385
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                                                                                                                                                                                                                              New Jersey
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                                                                                                                                                                                                                                                                                                                                                                                         , Susan E.
                                                                                                                                                                                                                                                                                                                                       useful therein
                                                                                                                                                                                                                                                                                                                                                          Cloning of the biosynthetic pathway for chlortetracycline and tetracyline Formation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US 07/874,166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1283;
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US-08-474-933-1/c
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TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 77; Conserv
                                                                                                                                                  APPLICATION NUMBER: US/08/474,933
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,468
FILING DATE: 22-5EP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                             NAME: Tsevdos, Estelle J
REGISTRATION NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31,255-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201,831-3241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14644 CAGCCGGTAGGAGTCGGCC 14626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14704 CCCCTGGCCGCCGGCCAGGTGGATGTGCGCGGCGTCGCCGGCCAGCAGCACCCGGCC 14645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 30001 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 quence 1, Application US/08474933 tent No. 5866410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Cloning of the biosynthetic pathway for TITLE OF INVENTION: chlortetracycline and tetracyline formation and cosmids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ryan, Michael J.
APPLICANT: Lotvin, Jason A.
APPLICANT: Strathy, Wancy
APPLICANT: Fantini, Susan E.
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REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201,831-3241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: One Cyanamid Plaza CITY: Wayne
                                                                                                                                                                                                                                                                                                                                                                                                                                               New Jersey
                                 (201)831-3305
                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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STRANDEDNESS: sing:
TOPOLOGY: linear
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Search completed: May 2, 2003, 09:34:38
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ALIGNMENTS

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Yamamoto, Hiroaki

APPLICANT: Onodera, Keiko

APPLICANT: Tani, Yoshiki

TIILE OF INVENTION: NOVEL (R)-2,3-BUTANEDIOL DEHYDROGENASE

FILE REFERENCE: 06501-092001

CURRENT APPLICATION NUMBER: US/10/020,674

CURRENT FILING DATE: 2002-04-19

PRIOR APPLICATION NUMBER: JP 2000-333363

PRIOR FILING DATE: 2000-10-31

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1143

TYPE: DA
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US-10-020-674-8
; Sequence 8, Application US/10020674
; Patent No. US20020160468A1
GENERAL INFORMATION:
APPLICANT: Yamamoto,
APPLICANT: Onodera, Keiko
APPLICANT: Tani, Yoshiki
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FILE REFERENCE: 06501-092001
CURRENT APPLICATION NUMBER: US/10/020,674
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: JP 2000-333363
PRIOR FILING DATE: 2000-10-31
PRIOR FILING DATE: 2000-10-31
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LENGTH: 530
; TYPE: DNA
; ORGANISM: Pichia &
US-10-020-674-8
APPLICANT: YOMANOCO, Hiroaki
APPLICANT: Onodera, Keiko
APPLICANT: Tani, Yoshiki
TITLE OF INVENTION: NOVEL (R)-2,3-BUTANEDIOL DEI
FILE REFERENCE: 06501-092001
CURRENT APPLICATION NUMBER: US/10/020,674
CURRENT FILING DATE: 2002-04-19
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: JP 2000-333363
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 706
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US-10-020-674-12
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Best Local :
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                                                                                                                                                               Sequence 12, Application US/10020674 Patent No. US20020160468A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 AAACCTGGTGACAGAGTCGCAGTTGAAGCTACGTCGCATTGCTCCGACAGATCGCGCTAC
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Pred. No. 4.6e-164;
0; Mismatches 7;
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GENERAL INFORMATION:

APPLICANT: Yanamoto, Hiroaki
APPLICANT: Onodera, Keiko
APPLICANT: Tani, Yoshiki
ITITLE OF INVENTION: NOVEL (R)-2,3-BUTANEDIOL DEHYDROGENASE
FILE REFERENCE: 06501-092001
CURRENT APPLICATION NUMBER: US/10/020,674
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: JP 2000-333363
PRIOR APPLICATION NUMBER: JP 2000-333363
PRIOR FILING DATE: 2000-10-31
SOFTWARE: FASTSEQ FOR WINDOWS Version 4.0
SEQ ID NO 15
SEQ ID NO 15
LENGTH: 523
TYPE: DNA
CONSTRUCT
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; ORGANISM: P10
US-10-020-674-12
                                                                                                                       Matches
                                                                                                                                Query Match
Best Local
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Patent No. US20020160468A1
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Best Local Similarity 99.8%;
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                                                                      TCGCCGTCAATGTGGCCGTTTGGGGAGACCACCCAATTGGATTCATGCCAATGTCTCTGA 919
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                                                                                                                           Score 328; DB 9; L; Pred. No. 1.9e-100;
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Pred. No. 1.4e-125;
0; Mismatches 1;
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APPLICANT: Kimoto, No. US20030032153A11h1ro

APPLICANT: Kimoto, No. US20030032153A11h1ro

ITILE OF INVENTION: NOVEL (R)-2,3 BUTARBDIOL DEHYDROGENASE,

ITILE OF INVENTION: METHODS FOR PRODUCING SAME, AND METHODS FOR PRODUCING

ITILE OF INVENTION: OPTICALLY ACTIVE ALCOHOL USING THE DEHYDROGENASE

FILE REFERENCE: 06501-109001

CURRENT APPLICATION NUMBER: US/10/147,003

CURRENT FILING DATE: 2002-05-16

PRIOR APPLICATION NUMBER: JP 2001-159647

PRIOR APPLICATION NUMBER: JP 2001-159647

PRIOR FILING DATE: 2001-05-28

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSEQ for Windows Version 4.0

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US-10-147-003-1
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Best Local Similarity 56.3
... 638; Conservative
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               421 TTGGGTGGTGCCAGCGGCGGTTTTGCCGAGTACGTCGTTTACGGTGAGGACCACATAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGAAAGGTTTACTTTACTTACGGTACAAACGATATTCGCTACTCCGAAACGGTTCCTGAA
CTAGGAGTTCACAGTGGTGGTTTTGCTGAAAAAGTCGTTGTTAGTGAAAAAGCACGTTGTT
                                                               GAATGTGCTGCTTGTCAAAGAGGGTTCTACAACTGTTGTGCCCCATTTGGGTTTCATGGGT
                                                                                  CTCTGTATGGCCTGCCAGAGCGGATCTCCGAACTGCTGTGCGTCGCTGAGCTTCTGCGGT 420
                                                                                                                                                            GCTACGTCGCATTGCTCCGACAGATCGCGCTACAAGGACACGGTCGCCCAAGACCTTGGG 360
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                                                                                                                                                                                       GTATCAAAAGTTGGACCAAAAGTAACCAACATCAAGGCTGGTGATCATGTTGTTGTAGAA
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                                                                                                                             GCCACCGGTACATGTCTTGATCATTACACTTGGCCTAACGCTGCACATGCTAAGGATGCT
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Pred. No. 1.2e-96;
0; Mismatches 486;
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TITLE OF INVENTION: MOVEL (R)-2,3-BUTANEDIOL DEHYDROGENASE,
TITLE OF INVENTION: MCYPEL (R)-2,3-BUTANEDIOL DEHYDROGENASE,
TITLE OF INVENTION: MCYPEL (R)-2,3-BUTANEDIOL DEHYDROGENASE,
TITLE OF INVENTION: MCYPHODS FOR PRODUCING SAME, AND METHODS FOR PRODUCING
FILE REFERENCE: 06501-109001
CURRENT APPLICATION NUMBER: US/10/147,003
CURRENT FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: US/10/147,003
PRIOR APPLICATION NUMBER: US/10/147,003
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
Type: Dana
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US-10-147-003-7
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                                                                   ; TYPE: DNA
; ORGANISM: Kluyveromyces aestuarii
US-10-147-003-7
                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/10147003
Publication No. US20030032153A1
GENERAL INFORMATION:
APPLICANT: Yamamoto, Hiroaki
APPLICANT: Kimoto, No. US20030032
Query Match 16.9
Best Local Similarity 55.4
Matches 397; Conservative
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              16.9%;
Score 193.2; DB Pred. No. 1e-54; 0; Mismatches 3
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RESULT 7

(US-10-020-674-11

(Sequence 11, Application US/10020674

; Patent No. US20020160448A1

GENERAL INFORMATION:
 APPLICANT: Yamamoto, Hiroaki
 APPLICANT: Onodera, Keiko
 APPLICANT: Onodera, Keiko
 APPLICANT: Tani, Yoshiki
 TITLE OF INVENTION: NOVEL (R)-2,3-BUTANEDIOL DEHYDROGENASE
 FILE REFERENCE: 06501-092001

CURRENT APPLICATION NUMBER: US/10/020,674

CURRENT FILING DATE: 2002-04-19

PRIOR FILING DATE: 2000-10-31

NUMBER OF SEQ ID NOS: 17

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 11

LENGTH: 107

TYPE: DNA

ORGANISM: Pichia angusta

US-10-020-674-11

Ouery Match
 Best Local Similarity 100.0%; Pred. No. 1.2e-24;
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RESULT 9
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US-09-891-641-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ye, Rick
APPLICANT: Bedzyk, Laura
APPLICANT: Bedzyk, Laura
APPLICANT: Wang, Tao
APPLICANT: WANG, Tao
TITLE OF INVENTION: NATURAL PROMOTERS FOR GENE EXPRESSION IN BACILLUS SPECIES
FILE REFERENCE: CL1686 US NA
CURRENT FILING NUMBER: US/09/891,641
CURRENT FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Microsoft 97
SEQ ID NO 11
LENGTH: 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                          GACAAGCCATCCAGTCCACTACAATTGCCGGTGAAACCGTCATCGTCAGCATTTGGGAAA
                                                                                                                                                                            CCACCTCAATTGTCGCCACGGGACCTTCTGGAATCGCCGTCAATGTGGCCGTTTGGGGAG 886
                                                                                                                                                                                                                                  TGCCGGAGAACGAGGGGATTCCATGCAGCCTTCGACTCTGGTGTTCCTCAGACATTCA 826
                                                                                                                                                                                                                 AACGTACAGGAGGCGGTGTTGACGTAGCATTCGAAGTCACTGGTGTCCCAGTGGTGTTAC
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Pred. No. 2.7e:
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; LOCATION: (1)...(1092)
US-09-815-242-7881
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
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SOFTWARE: FastSEQ for Windows Version SEQ ID NO 7881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.6%;
Best Local Similarity 46.5%;
Matches 326; Conservative
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Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
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ORGANISM: Pseudomonas aeruginosa
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                                 792 AGCCTTCGACTGCTCTGGTGTTCCTCAGACATTCACCACCTCAATTGTCGCCACGGGACC
                                                                                  705
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CAGCTTCGAATGCATCGGCAACAAGCACACCGCCAAGCTGGCCATCGATGCCATCCGCAA 821
                                                                                                           ATGTGACGACGCAAATGCTGTTCTCAAGGCTATGGTGCCGGAGAACGAGGGATTCCATGC
                                                                        GCGGTGCGACGCCCTAGGCGAAATCCGCGC---CCTCACCGGCGGGCTTGGCGCCGACGT
                                                                                                                                                GTCCTCGGCGCAAGGCCAAGGCCCTGGAGGTCGGCGAGCCAGGTGCTCGACCCCTC
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Zyskind, Judith W.
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Pred. NO. 8.7e-11;
0; Mismatches 357;
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US-09-925-300-386
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NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 386
LENGTH: 2410
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APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: n equals a,t,g, or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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                                                                                                                     660 GTGTTCCGAGCCGGCCTTGATCAGAAGACAGTTTGCAAAGGAACTGGGCGCTGAAGTGTT 719
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les 123; Conserv
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                                                                              GGTGACTGATCTGCTACCCGATTGTCCAAAGCCAAGGAGATTGGGGCTGATTTAGT 660
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nilarity 51.0%;
Conservative
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1.2e-06;
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RESULT 11
US-09-969-708-281
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US-09-969-708-281
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APPLICANT: Augustus, Meena
APPLICANT: Augustus, Meena
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
TITLE OF INVENTION: Sets
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SEQ ID NO 281
LENGTH: 2519
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                                                                                                                                                                                                                                                                                                                            Sequence 2189, Application US/09880107 Patent No. US20020142981A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 123; Conserv
SEQ ID NO 2189
LENGTH: 2519
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PRIOR FILING DATE: 2000-10-03
PRIOR PPLICATION NUMBER: US/60/237,608
PRIOR FILING DATE: 2000-10-03
PRIOR PPLICATION NUMBER: US/60/237,425
PRIOR FILING DATE: 2000-10-03
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CURRENT APPLICATION NUMBER: US/09/969,708
CURRENT FILING DATE: 2001-10-03
                                                                           PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
                                                                                                                                                             TITLE OF INVENTION: Gene Expression Profiles FILE REFERENCE: 44921-5028-WO CURRENT APPLICATION NUMBER: US/09/880,107 CURRENT FILING DATE: 2001-06-14
                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 658
                                        SOFTWARE: PatentIn Ver.
                                                              NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                         APPLICANT: Horne,
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Pred. No. 1.2e-06;
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US-09-974-300-551
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                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 139; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Berks, Randy M.
APPLICANT: Clausen, Ib Groth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. US20020146721a1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity Matches 123; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens FEATURE:
                                                                                                        328
                                                                                                                             418
                                                                                                                                                      268
                                                                                                                                                             358 GGGCTCTGTATGGCCTGCCAGAGCGGATCTCCGAACTGCTGTGTGCGTTGAGCTTCTGC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   800 C 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           740 GGTGACTGATCTGTCTGCTACCCGATTGTCCAAAGCCAAGGAGATTGGGGGCTGATTTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   660 GTGTTCCGAGCCGGCCTTGATCAGAAGACAGTTTGCAAAAGGAACTGGGCGCTGAAGTGTT
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GGCGCCCACGCTGCAGAAAGGGCAAATATCAAAAAAGGGGAAACGGTGCTTGTTGGA
                GCCTGGCATGCTGTTGAACGCGCTAGATTCCAGCCTGGTCAGACGGCCCTGGTTCTTGGA 597
                                               CTAAAAACAGAAGGATTGACGCTCAGCGA---AGCTGCTGTTGTTGAATGTTTAAGCATC
                                                                 GTCAAGCTGCCAGACTCGATTCCCGACGATATTGGAGCACTGGTTGAGCCTATTTCTGTT
                                                                                               GGT----GTCCATACAGACGGGGAATGCGGGAATACATAAACGTCCCGGCAGACCACCTG
                                                                                                              GGTTTGGGTGGTGCCAGCGGCGGTTTTGCCGAGTACGTCGTTTACGGTGAGGACCACATG
                                                                                                                                              GGGCATGCATCGCCTGCCGGAACGGACGCCCCAACTGCTGCGTCAATCTGAACGTCCTC.
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                                                                                                                                                                                                  Conservative
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Pred. No. 1.2e-06;
0; Mismatches 118;
                                                                                                                                                                                                             Score 45.8; DB 10;
Pred. No. 0.0001;
                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     Multiple
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                                                                                                                                                                                                                       Length 1014;
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                                                                                                                  RESULT 15
US-09-922-217-153
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GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun APPLICANT: Lodes, Michael J.

APPLICANT: APPLICANT: APPLICANT:

Stolk, Ju... Mang, Tongtong

Meagher, Madeleine Joy Secrist, Heather Benson, Darin R. Sequence 153, Application US/09922217 Patent No. US20020076414A1

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APPLICANT: King, Gordon E.

APPLICANT: Wang, Aijun

APPLICANT: Clapper, Jonathan D.

APPLICANT: Skeiky, Yasir A. W.

APPLICANT: Skeiky, Yasir A. W.

APPLICANT: Skeiky, Yasir A. W.

APPLICANT: Fanger, Gary R.

APPLICANT: Carter, Darrick

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS

TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.471C14

CURRENT FILING DATE: 2001-12-19

INUMBER OF SEQ ID NOS: 1129

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 153

LENGTH: 513

TYPE: DNA

ORGANISM: Homo sapiens
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US-10-025-380-153
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Best Local Similarity 51.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                           660 GIGITCCGAGCCGGCCTTGATCAGA 684
                                                             424 TGGGCCAATCGGGATGGTCACTTTGCTCGTGGCCAAAGCAATGGGAGCAGCTCAAGTAGT
 484
                                                                                                                              304 CAAGCTTCCTGACAATGTCACCTTTGAGGAAGGCGCCCTGATCGAGCCACTTTCTGTGGG
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                                                                                             AGGTCCTATCGGCCTTGCCACCATTCTTGCTCTGCAAGGCCATCATGCGGGCAAAATTGT
                                                                                                                                                                 CTGGCATGCTGTTGAACGCGCTAGATTCCAGCCTGGTCAGACGGCCCTGGTTCTTGGAGG
GGTGACTGATCTGTCTGCTACCCGA 508
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Smith, Carole L.
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Benson, Darin R.
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Pred. No. 0.00013;
0; Mismatches 100
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APPLICANT: Jiang, Yuqiu
APPLICANT: Smith, Carole Lynn
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: OF COLON FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 153
ILENGTH: 513
TYPE: DNA
ORGANISM: Homo sapiens
US-09-922-217-153
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Search completed: May 2, 2003, 12:08:43
Job time: 177 secs
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Best Local Similarity 51.2%;
Matches 105; Conservative
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                                                                                     484 GGTGACTGATCTGTCTGCTACCCGA 508
                                                                                                                                660 GTGTTCCGAGCCGGCCTTGATCAGA 684
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